

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 02:08:58 ; Search time 51 Seconds

(without alignments)  
3589.922 Million cell updates/sec

Title: US-09-575-580B-2

Perfect score: 597

Sequence: 1 atggaggagggtgactgca.....caccgatccaccttagctga 597

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

- 1: /cgn2\_6ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	398	66.7	2174	2 US-08-665-040-1	Sequence 1, Appli
2	38.4	6.4	3303	1 US-08-081-610-3	Sequence 3, Appli
3	37.8	6.3	7218	1 US-08-232-463-14	Sequence 14, Appl
4	37.6	6.3	7130	4 US-09-056-105-31	Sequence 31, Appl
5	37.2	6.2	50937	4 US-09-428-517-1	Sequence 1, Appli
6	36.2	6.1	6328	4 US-08-913-832A-1	Sequence 1, Appli
7	36.2	6.1	6328	4 US-09-249-181A-1	Sequence 1, Appli
8	36	6.0	911	2 US-08-924-759-9	Sequence 9, Appli
9	36	6.0	911	3 US-09-248-335-9	Sequence 9, Appli
10	34	5.7	1296	1 US-07-816-283-9	Sequence 9, Appli
11	34	5.7	1296	1 US-08-417-103-9	Sequence 9, Appli
12	34	5.7	2118	4 US-09-221-017B-789	Sequence 789, App
13	33.2	5.6	2277	1 US-08-676-967-2	Sequence 2, Appli
14	33.2	5.6	2277	1 US-08-676-974-2	Sequence 2, Appli
15	33.2	5.6	2277	2 US-09-098-487-2	Sequence 2, Appli
16	33.2	5.6	2289	4 US-09-312-038-3	Sequence 3, Appli
17	33	5.5	2089	1 US-08-552-142A-1	Sequence 1, Appli
18	33	5.5	2089	4 US-09-910-973-1	Sequence 1, Appli
19	33	5.5	2089	4 US-09-499-227-1	Sequence 1, Appli
20	33	5.5	2089	5 PCT-US95-05741-1	Sequence 1, Appli
21	33	5.5	4221	4 US-09-651-656-22	Sequence 22, Appl
22	33	5.5	4221	4 US-09-650-855-22	Sequence 22, Appl
23	32.4	5.4	602	4 US-09-470-191-81	Sequence 81, Appl
24	32.4	5.4	21338	4 US-08-961-527-20	Sequence 20, Appl
25	32.2	5.4	435	4 US-09-397-787-282	Sequence 282, App
26	32	5.4	16442	3 US-08-781-891-208	Sequence 208, App
27	31.8	5.3	3489	2 US-08-728-323A-1	Sequence 1, Appli

28	31.8	5.3	3489	4 US-09-298-568-1	Sequence 1, Appli
29	31.8	5.3	32207	2 US-08-770-379-20	Sequence 20, Appl
30	31.8	5.3	32207	4 US-08-757-669A-20	Sequence 20, Appl
31	31.8	5.3	32207	4 US-09-230-371A-20	Sequence 20, Appl
32	31.6	5.3	7015	4 US-09-177-249-6	Sequence 6, Appli
33	31.6	5.3	36519	3 US-08-923-137-2	Sequence 3, Appli
34	31.2	5.2	16389	4 US-09-741-154-3	Sequence 16, Appl
35	31	5.2	1462	1 US-08-552-142A-16	Sequence 1, Appli
36	31	5.2	1930	2 US-08-737-716-1	Sequence 1, Appli
37	31	5.2	1930	2 US-08-737-716-11	Sequence 11, Appl
38	31	5.2	1951	1 US-08-910-973-16	Sequence 16, Appl
39	31	5.2	1951	4 US-09-499-227-16	Sequence 16, Appl
40	31	5.2	15378	3 US-08-785-420-1	Sequence 1, Appli
41	30.8	5.2	1155	4 US-08-818-111-12	Sequence 12, Appl
42	30.8	5.2	1155	4 US-08-818-111-12	Sequence 12, Appl
43	30.8	5.2	1155	4 US-09-056-556-12	Sequence 12, Appl
44	30.8	5.2	1155	4 US-09-072-596-12	Sequence 12, Appl
45	30.8	5.2	28720	4 US-09-341-587-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-08-665-040-1  
; Sequence 1, Application US/08665040  
; Patent No. 5869318  
; GENERAL INFORMATION:  
; APPLICANT: ESTIVILL PALLEJA, XAVIER  
; APPLICANT: FUENTES, JUAN JOSE  
; APPLICANT: PRITCHARD, MELANIE  
; TITLE OF INVENTION: A NEW GENE SEQUENCE OF THE  
; TITLE OF INVENTION: DOWN SYNDROM CRITICAL REGION OF HUMAN CHROMOSOME 21,  
; TITLE OF INVENTION: IDENTIFIED BY A NEW "ALU-SPlicing PCR" TECHNIQUE,  
; TITLE OF INVENTION: CODING FOR A PROLINE-RICH PROTEIN (DSCR1) HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN FOETEL BRAIN AND IN HEART AND METHOD  
; TITLE OF INVENTION: FOR CHARACTERIZING IT.  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LADAS & PARRY  
; STREET: 26 WEST 61ST STREET  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10023  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT 5.1 FOR DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,040  
; FILING DATE: JUNE 7, 1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: ES P9501140  
; FILING DATE: JUNE 7, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JANET I. CORD  
; REGISTRATION NUMBER: 33,778  
; REFERENCE/DOCKET NUMBER: U010815-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 708-1800  
; TELEFAX: (212) 246-8959  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2174 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA for mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

us-09-575-580b-2.rni

Fri Nov 15 07:56:45 2002

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ORIGINAL SOURCE: human
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: foetal
TISSUE TYPE: Brain
IMMEDIATE SOURCE: gene library of cDNA
LIBRARY: gene library of cDNA from foetal
CLONE: BC-17.8-1 and BC-17.8-2
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 21/YAC 72H9
MAP POSITION: 21q22.1-q22.2
FEATURE:
NAME/KEY: cDNA for mRNA, BC-17.8
LOCATION: 1..2174
FEATURE:
NAME/KEY: untranslated 5'
LOCATION: 1..48
FEATURE:
NAME/KEY: coding sequence
LOCATION: 49..560
OTHER INFORMATION: Down Syndrome critical
FEATURE:
NAME/KEY: DSCR1
LOCATION: 1..171 PEPTIDES
IDENTIFICATION METHOD: translation of the
OTHER INFORMATION: - deduced protein
OTHER INFORMATION: - proline-rich protein domains
OTHER INFORMATION: - glutamic acid-rich protein domains
OTHER INFORMATION: - leucine/phenylalanine-rich protein domains
FEATURE:
NAME/KEY: untranslated 3'
LOCATION: 564..2174
FEATURE:
NAME/KEY: 2 poly (A)
LOCATION: 1541..1546 AND 2132..2137
US-08-665-040-1
Query Match 66.7%; Score 398; \ DB 2; Length 2174;
Best Local Similarity 87.6%; Pred. No. 2.3e-109;
Matches 447; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 88 GCCAAATTTGAATCCCTCTTCAGACATATGACAGGACACACCTTCCAGTATTTTAAAG 147
DB 58 GCCAAATTTGAGTCCCTCTTTAGGACGTATGACAGGACATCACCTTTTCAGTATTTTAAAG 117
QY 148 AGCTTCAACAGTGTCCGGATAAATTCAGAACCCCTTATCTGCGAGCGATGCCAGGCTG 207
DB 118 AGCTTCAACAGTGTGAGTAAATTCAGAACCCCTTATCTGCGAGGAGATGCCAGGCTC 177
QY 208 CGGTGTCACAGACCGAGTTCCTGGGGAAGAAATGAAGTTGATTTTGGCTCAGACTTA 267
DB 178 CAGCTGCAATAGACTGAGTTCTGGGGAAGAAATGAAGTTGATTTTGGCTCAGACTTA 237
QY 268 CACATAGGAAGTTACACCTGGTCCGCCCAATCCGACAAACAGTTCTCATCTCCCT 327
DB 238 CACATAGGAAGTTACACCTGGTCCGCCCAATCCGACAAACAGTTCTCATCTCCCT 297
QY 328 CGGCTCTCTCTCCCTGGTGGTGGGAACAAAGTAGAAGATGCCACCCCGTCAATAATTAC 387
DB 298 CGGCTCTCTCTCCCTGGTGGTGGGAACAAAGTAGAAGATGCCACCCCGTCAATAATTAC 357
QY 388 GATCTTTTATATGCCATCTCCAAAGTGGGCGGAGAGAGATGATGAATGCGATGCGAGCG 447
DB 358 GATCTTTTATATGCCATCTCCAAAGTGGGCGGAGAGAGATGATGAATGCGATGCGAGCG 417
QY 448 ACAGACCCACTCCAGTGTGTGTCACGTTGTCAGAGTGTGTCAGAGTGTGTCAGAGTGTGTCAGAG 507
DB 418 ACTGACACCACTCCAGTGTGTGTCACGTTGTCAGAGTGTGTCAGAGTGTGTCAGAGTGTGTCAGAG 477
QY 508 GAAGAGGAAGATGAGAGAGATGAGAGACCAAGCCCAAAATCATCCAGACACGGAGA 567
DB 478 GAAGAGGAA---ATGGAAGAAATGAGAGAGACCTTAAGCCCAAAATTTATCCAGACCAAGGAGG 534

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QY 568 CCGGAGTACACGCGATCCACCTTAGCTGA 597
DB 535 CCGGAGTACACGCGATCCACCTTAGCTGA 564

RESULT 2
US-08-081-610-3
Sequence 3, Application US/08081610
Patent No. 5445941
GENERAL INFORMATION:
APPLICANT: Yang, Na N
TITLE OF INVENTION: Materials and Methods for Screening
Anti-Osteoporosis or Serum Lipid Lowering Agents
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti and Witcoff, Ltd.
STREET: 10 S. Wacker Dr.
CITY: Chicago
STATE: IL
COUNTRY: U.S.A
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/081,610
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heahy, Barbara A
REGISTRATION NUMBER: 34,619
REFERENCE/DOCKET NUMBER: 93,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3303 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: mRNA
LOCATION: 2170..3303
FEATURE:
NAME/KEY: mRNA
LOCATION: 2214..3303
FEATURE:
NAME/KEY: mRNA
LOCATION: 2219..3303
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 3301..3303
OTHER INFORMATION: /note= "CDS Start, codon start = 1,
OTHER INFORMATION: translation M"
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 2170..2176
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1896..2306
OTHER INFORMATION: /note= "pb-301 -301 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1976..2306
OTHER INFORMATION: /note= "pb-221 -221 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2106..2306
OTHER INFORMATION: /note= "pb-91 -91 to +110"

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; GENERAL INFORMATION:  
; APPLICANT: Betlach, Mary C.  
; APPLICANT: Shah, Sanjay Krishnakant  
; APPLICANT: McDaniel, Robert

us-09-575-580b-2.rni

Fri Nov 15 07:56:45 2002

```

; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 50937
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant DNA
US-09-428-517-1

Query Match          6.1%; Score 37.2; DB 4; Length 50937;
Best Local Similarity 56.6%; Pred. No. 0.63; Indels 0; Gaps 0;
Matches 69; Conservative

QY 2 TGGAGGAGTGGATCTGCAGGACCTGCGGAGCGCCACCATCGCTGCCACTGGACCCGC 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8767 TGACGGCGCTGGAACCTGCGGAGCGCTCGACACCGCACTCGGCTCGCTGCCACGCA 8826
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 CGGTGTTCTGGAGCGCTGTCGCGGCGCCAAATTTGAATCCCTCTTCAGAACATATGACA 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8827 GCGTGTCTTCGACCAACCGCCAGCCCGCGGCGCACTGGCAGCGTCTCTCCAGGGCGCAGCA 8886
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 AG 123
Db 8887 CG 8888

RESULT 6
US-08-913-832A-1
; Sequence 1, Application US/08913832A
; Patent No. 6329517
; GENERAL INFORMATION:
; APPLICANT: Seelig, Hans Peter
; APPLICANT: Renz, Manfred
; TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
; FILE REFERENCE: 8484-0030-999
; CURRENT APPLICATION NUMBER: US/08/913,832A
; CURRENT FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: PCT/DE96/00444
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6328
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5736)
US-08-913-832A-1

Query Match          6.1%; Score 36.2; DB 4; Length 6328;
Best Local Similarity 53.1%; Pred. No. 0.5; Indels 0; Gaps 0;
Matches 77; Conservative

QY 421 GGAGAGAGTATGAACCTGCATCGAGCGACAGACCCCACTCCAGTGTGTGTCACGCGT 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4921 GTAGAGAAAGTGGAGGAAAGTCTAGCAATAGATCTGACCCCTATTGTGTAGACACAA 4980
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 TGTGAGAGTGCACCAAGAGAGATGAGGAGAGAGAGAGATGAGAGAGATGAGAGAGAG 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4981 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 AAGCCCAAAATCATCCAGACACGGA 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5041 AAGGACCTGATGATGAGAGAAACAGA 5065
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-08-924-759-9
; Sequence 9, Application US/08924759
; Patent No. 5962229
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,759
; FILING DATE:
; CLASSIFICATION: 435

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Db 5041 AAGGACCTGATGATGAGAGAAACAGA 5065
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RESULT 7
US-09-249-181A-1
; Sequence 1, Application US/09249181A
; Patent No. 6440679
; GENERAL INFORMATION:
; APPLICANT: Seelig, Hans Peter
; APPLICANT: Renz, Manfred
; TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
; FILE REFERENCE: 8484-0059-999
; CURRENT APPLICATION NUMBER: US/09/249,181A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/913,832
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: PCT/DE96/00444
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6328
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5736)
US-09-249-181A-1

Query Match          6.1%; Score 36.2; DB 4; Length 6328;
Best Local Similarity 53.1%; Pred. No. 0.5; Indels 0; Gaps 0;
Matches 77; Conservative

QY 421 GGAGAGAGTATGAACCTGCATCGAGCGACAGACCCCACTCCAGTGTGTGTCACGCGT 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4921 GTAGAGAAAGTGGAGGAAAGTCTAGCAATAGATCTGACCCCTATTGTGTAGACACAA 4980
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 TGTGAGAGTGCACCAAGAGAGATGAGGAGAGAGAGAGATGAGAGAGATGAGAGAGAG 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4981 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 AAGCCCAAAATCATCCAGACACGGA 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5041 AAGGACCTGATGATGAGAGAAACAGA 5065
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-08-924-759-9
; Sequence 9, Application US/08924759
; Patent No. 5962229
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,759
; FILING DATE:
; CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0184
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 911 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: MAIZE
; IMMEDIATE SOURCE:
; CLONE: CC/ISE-B.PK0014.B8
; US-08-924-759-9
;
; Query Match 6.0%; Score 36; DB 2; Length 911;
; Best Local Similarity 56.9%; Pred. No. 0.24;
; Matches 66; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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; Qy 22 GACCTGCGGAGCGGCACCATCGCTGCCACCTGGACCGCGGTGTTGTTGACGGCCTG 81
; Db 144 GAGCTCTGCTCCACCACACCCCGTGACAGAGGTGCCGCTGCTCTCCACGGCGAC 203
;
; Qy 82 TCCCGGGCCAAATTGTAATCCTCTTTCAGAACATATGACAGGACACACCTTCCA 137
; Db 204 GCGCGGGCCATCTCGGAGTCCCTGCTCATCGCCGAGTACGTGCGAGAGGCTTCGA 259
;
; RESULT 9
; US-09-248-335-9
; Sequence 9, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 9
; LENGTH: 911
; TYPE: DNA
; ORGANISM: maize
; US-09-248-335-9
;
; Query Match 6.0%; Score 36; DB 3; Length 911;
; Best Local Similarity 56.9%; Pred. No. 0.24;
; Matches 66; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
;
; Qy 22 GACCTGCGGAGCGGCACCATCGCTGCCACCTGGACCGCGGTGTTGTTGACGGCCTG 81
; Db 144 GAGCTCTGCTCCACCACACCCCGTGACAGAGGTGCCGCTGCTCTCCACGGCGAC 203
;
; Qy 82 TCCCGGGCCAAATTGTAATCCTCTTTCAGAACATATGACAGGACACACCTTCCA 137
; Db 204 GCGCGGGCCATCTCGGAGTCCCTGCTCATCGCCGAGTACGTGCGAGAGGCTTCGA 259
;
; RESULT 10
; US-07-816-283-9
; Sequence 9, Application US/07816283
; Patent No. 5436155
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; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-816-283-9
;
; Query Match 5.7%; Score 34; DB 1; Length 1296;
; Best Local Similarity 56.1%; Pred. No. 1.1;
; Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
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; Qy 469 GTGGTCCAGCTGTGTGAGAGTACCACCAAGAAATGAGGAGAGAGAGAGAGAGAGA 528
; Db 1051 GTGGGGCCCCCGGAGAGACTGTGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGC 1110
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; Qy 529 ATGAAGAGACCCCAAGCCCCAAATCATCCAGACACGAGACCGGAGTACACACCG 582
; Db 1111 AGGGAGGGGGGCAAGGGAAGGAGATGAACGCGCGGTTCAGCCAGATCACGACG 1164
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; RESULT 11
; US-08-417-103-9
; Sequence 9, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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Fri Nov 15 07:56:45 2002

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APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 28...1281
US-08-417-103-9

Query Match
Best Local Similarity 56.1%; Pred. No 1:1;
Matches 64; Conservative 5.7%; Score 34; DB 1; Length 1296;

QY 459 GTGGTCCACCTGTGTGAGAGTACACCAAGAGAAATGAGGAGGAAGAGAGATGGAGAGA 528
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DB 1111 AGCGAGGGGGGCAAGGGGAGGAGGATGAACGGCCGGGTGACCCAGATCACCAG 1164
QY 529 ATGAAGAGACCCAGGCCCAAAATCATCCAGACACGAGACCGGGAGTACACCG 582
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RESULT 12  
US-09-221-017B-789/C  
; Sequence 789, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FAST-SEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: Pp1182  
; APPLICATION NUMBER: Pp1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA: Pp1546  
; APPLICATION NUMBER: Pp1546  
; FILING DATE: 30-JAN-1998  
; APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: Pp2911  
; FILING DATE: 09-APR-1998  
; PRIOR APPLICATION DATA: PCT/AU98/01023  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 789:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2118 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 1...2118

US-09-221-017B-789

Query Match 5.7% Score 34; DB 4; Length 2118;  
Best Local Similarity 57.5%; Pred. No. 1.4;  
Matches 61; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Db 1380 GAGTGTCTTATGTCTGAAGAAAATCCGTACCGCAGCTATGTAGACANTACAGGGGT 1321  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 207 GC GGCTGCACAAGCAGAGTTCCTGGGGAAGAATGAAGTTGTAT 252  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1320 TCGTGGCCAAGTCAGCGAAATCCTTGGCGAGAAATCAACTTTTTT 1275

RESULT 13  
US-08-676-967-2  
Sequence 2, Application US/08676967  
Patent No. 5747317  
GENERAL INFORMATION:  
APPLICANT: COLLINS, KATHLEEN  
TITLE OF INVENTION: Human Telomerase  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Science & Technology Law Group  
STREET: 268 Bush Street, Suite 3200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/676,967  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman Ph.D., Richard A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: UC896-055  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)343-4341  
TELEFAX: (415)343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2277 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

Db 728 ARGAYGGNNTTYYGAYGAYGARGARGARGARAYATHGARGWSNARGTGNACNA 787

Search completed: November 15, 2002, 03:30:28  
Job time : 83 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 00:52:13 ; Search time 2653 Seconds  
(without alignments)  
6548.954 Million cell updates/sec

Title: US-09-575-580B-2  
Perfect score: 597  
Sequence: 1 atgaggaggatggatctgca.....caccgatccaccttaqctga 597

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_yi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_on:\*  
21: em\_or:\*  
22: em\_ov:\*  
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24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rod:\*  
36: em\_hcg\_mam:\*  
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39: em\_hcg\_hum:\*  
40: em\_hcg\_mus:\*  
41: em\_hcg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	597	100.0	597	6	AX365312	AX365312 Sequence
2	597	100.0	597	10	AF237789	AF237789 Mus muscu
3	592.2	99.2	621	10	AF282255	AF282255 Mus muscu
4	592.2	99.2	2125	10	AF260717	AF260717 Mus muscu
5	515.8	86.4	597	6	AX365315	AX365315 Sequence
6	515.8	86.4	597	10	AF237790	AF237790 Mus muscu
7	511	85.6	2141	10	AF263239	AF263239 Mus muscu
8	511	85.6	2198	10	BC013551	BC013551 Mus muscu
9	507.2	85.0	2224	10	AF263240	AF263240 Mus muscu
10	481.8	80.7	2212	6	AX365324	AX365324 Sequence
11	481.8	80.7	2227	9	HSU85266	HSU85266 Homo sapien
12	481.8	80.7	2289	9	BC002864	BC002864 Homo sapi
13	481.8	80.7	2407	9	AK092184	AK092184 Homo sapi
14	430.8	72.2	626	10	AB075973	AB075973 Rattus no
15	427.8	71.7	2216	10	CGU60263	US0263 Cricetulus
16	426.2	71.4	599	6	AX365311	AX365311 Sequence
17	403.8	67.6	2331	6	AX365321	AX365321 Sequence
18	403.8	67.6	2346	9	HSU85267	HSU85267 Homo sapien
19	401.6	67.3	2284	9	HSU85265	HSU85265 Homo sapien
20	399.6	66.9	2173	6	AX410694	AX410694 Sequence
21	399.6	66.9	2173	9	HSU28833	U28833 Homo sapien
22	399.6	66.9	2679	9	AK055845	AK055845 Homo sapi
23	398	66.7	798	9	AF400429	AF400429 Homo sapi
24	398	66.7	2174	6	AR034241	AR034241 Sequence
25	392.8	65.8	2348	9	AX281651	AX281651 Sequence
26	335	56.1	562	9	HSU52821	US3821 Homo sapien
27	211	35.3	934	6	AX074351	AX074351 Sequence
28	211	35.3	3159	6	AX420425	AX420425 Sequence
29	211	35.3	3261	9	AK090990	AK090990 Homo sapi
30	207.8	34.8	3240	9	AY034085	AY034085 Homo sapi
31	207.8	34.8	3253	9	AY034086	AY034086 Homo sapi
32	195.6	32.8	3295	10	AB061525	AB061525 Mus muscu
33	193	32.3	3184	6	AX329596	AX329596 Sequence
34	193	32.3	3184	6	AX333015	AX333015 Sequence
35	193	32.3	3184	6	AX365327	AX365327 Sequence
36	193	32.3	3184	6	AX420436	AX420436 Sequence
37	193	32.3	3184	6	H0MZAK14	D83407 ZAK1-4 mrNA
38	186.4	31.2	720	6	AX365333	AX365333 Sequence
39	186.4	31.2	720	6	AF176117	AF176117 Homo sapi
40	186.4	31.2	828	6	AX365330	AX365330 Sequence
41	186.4	31.2	828	6	AX420437	AX420437 Sequence
42	186.4	31.2	828	6	AF176116	AF176116 Homo sapi
43	184.6	30.9	615	6	AX420432	AX420432 Sequence
44	183.2	30.7	794	10	AF237888	AF237888 Mus muscu
45	183	30.7	594	6	AX365318	AX365318 Sequence

## ALIGNMENTS

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Fri Nov 15 07:56:43 2002

[illegible]

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QY 541 AAGCCCAAAATATCCAGACACGGAGACGGAGTACACACCGATCCACCTTAGCTGA 597
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RESULT 3
AF282255 621 bp mRNA linear ROD 17-NOV-2000
LOCUS Mus musculus Down syndrome candidate region 1 protein (Dscr1) mRNA,
DEFINITION complete cds.
ACCESSION AF282255
VERSION AF282255.1 GI:9652249
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 621)
The murine DSCR1-like (Down syndrome candidate region 1) gene
family: conserved synteny with the human orthologous genes
JOURNAL Gene 257 (2), 223-232 (2000)
MEDLINE 20534792
PUBMED 11080588
REFERENCE 2 (bases 1 to 621)
AUTHORS Strippoli, P., Petrini, M., Lenzi, L., Carinci, P. and Zannotti, M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Istituto di Istologia ed Embriologia
Generale, Universite di Bologna, Via Belmeloro, 8, Bologna, BO
40126, Italy
FEATURES
Location/Qualifiers
Source 1..621
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="16"
/sex="male"
/tissue_type="brain"
1..621
/gene="Dscr1"
8..604
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/note="similar to the Homo sapiens Down syndrome candidate
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/codon_start=1
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/protein_id="AAF91461.1"
/db_xref="GI:9652250"
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BASE COUNT 166 a 179 c 159 g 117 t
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Best local Similarity 99.5%; Pred. No. 2.2e-147;
Matches 594; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 8 ATGGAGGAGTGGATCGAGGACCTGCGGAGCGGCCACCATCGCTGCCACCTGGACCG 67
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QY 61 CGCGTGTTCGTGGAGCGCTGTGCGGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 120
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Db 68 CGCGTGTTCGTGGAGCGCTGTGCGGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 127
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QY 121 AAGGACACACCTTCCAGTATTTAAGAGCTTCAACAGTGTCCGGATAAATTTACAGAAC 180
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Db 128 AAGGACACACCTTCCAGTATTTAAGAGCTTCAACAGTGTCCGGATAAATTTACAGAAC 187

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QY 181 CCCTATCTGCAGCGGATGCCAGGCTGCGGCTGCACAAGACCGAGTTCTTGGGAAGGAA 240
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QY 241 ATGAAGTGTATTTTGTCTCAGACTTTTACACATAGGAAGTTTACACCTGGCTCCGCCCAAT 300
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Db 248 ATGAAGTGTATTTTGTCTCAGACTTTTACACATAGGAAGTTTACACCTGGCTCCGCCCAAT 307
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QY 301 CCGGACAAACAGTTTCTCATCTCCCTCCGCGCTCTCTCCCGTTGGCTGGAAACAAGTA 360
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Db 308 CCGGACAAACAGTTTCTCATCTCCCTCCGCGCTCTCTCCCGTTGGCTGGAAACAAGTA 367
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QY 361 GAAGATGCCACCCCGCTCATAAATACGATCTTTTATATGCGCATCTCCCAAGCTGGGGCCA 420
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RESULT 4
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LOCUS Mus musculus Down syndrome candidate region 1 (Dscr1) mRNA, complete
DEFINITION cds.
ACCESSION AF260717
VERSION AF260717.1 GI:7839596
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 2125)
Casas, C., Martinez, S., Pritchard, M.A., Fuentes, J.J., Nadal, M.,
Guimera, J., Arbones, M., Florez, J., Soriano, E., Estivill, X. and
Alcantara, S.
Dscr1, a novel endogenous inhibitor of calcineurin signaling, is
expressed in the primitive ventricle of the heart and during
neurogenesis
Mech. Dev. 101 (1-2), 289-292 (2001)
JOURNAL 21152920
MEDLINE 11231093
PUBMED
REFERENCE 2 (bases 1 to 2125)
AUTHORS Fuentes, J.J., Pritchard, M., Pucharcas, C. and Estivill, X.
TITLE Down syndrome candidate region 1 (Dscr1), one of three
alternatively spliced exon 1
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2125)
AUTHORS Fuentes, J.J., Pritchard, M., Pucharcas, C. and Estivill, X.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2000) Centre de Genetica Medica i Molecular, IRO,
Avia, Castelldefels Km. 2,7, L'Hospitalet de Llobregat, Barcelona
08907, Spain
FEATURES
Location/Qualifiers
Source 1..2125
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="16"
1..2125
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us-09-575-580b-2.rge

Fri Nov 15 07:56:43 2002

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		/db_xref="GI:18697046"					
		/translation="MDRFQSYNFSLLACVANDVSESETRAKFESLERTYDKDPTT					
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		3 others					
BASE COUNT		487 a		536 c		536 t	
ORIGIN		170 a		156 c		142 g	
		129 t					
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Best Local Similarity		94.4%		Pred. No. 5.6e-127		Length 597	
Matches 535		Conservative		0		Mismatches 32	
		Indels 0		Gaps 0			
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Db		31		AGCTCCCTGATGCTGTGTGGCAACGATGATGCTTTCACGGAANGTGAGACCGGCC		90	
QY		91		AAATTTGAATCCCTCTTCAGAACATATGACAGGACACCACTTCCAGTATTTTAAAGAC		150	
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QY		151		TTCAACAGCTGCGGATAAATTCAGCAACCCCTTATCTGCAGCGGATGCCAGGCTGGG		210	
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Db		271		ATAGGAAGTTTCAACCTGCGCCCAATCCGACAAACAGTTCTCTATCTCCCTCCG		330	
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Db		331		GCCTCTCTCCCTGCTGGTGGAAACAAAGTAGAAGTGCACCCCGTCATAAATACGAT		390	
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Db		511		GAGGAGAGATGGAGAGATGAAGAGACCCAAAGCCCAAAATCATCCAGACGAGGACCG		570	
QY		571		GAGTACACACCGATCCACCTTAGCTGA		597	
Db		571		GAGTACACACCGATCCACCTTAGCTGA		597	
RESULT 6		AF237790		597 bp		linear	
LOCUS		AF237790		Mus musculus myocyte-enriched calcineurin interactin protein 1		linear	
DEFINITION		splice variant 4 mRNA, complete cds.					
ACCESSION		AF237790					
VERSION		AF237790.1		GI:7542528			
KEYWORDS		Mus musculus					
SOURCE		Mus musculus					
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					



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Db 361 GCCTCTCTCCCTGGCTGGGAACAAGTAGAAGATGCCACCCCGTCATAAATACGAT 420
Qy 391 CTTTATATGCACTCTCAAGCTGGGCGCAGGAGAGATGATGAACATGCATGCAGCGACA 450
Db 421 CTTTATATGCACTCTCAAGCTGGGCGCAGGAGAGATGATGAACATGCATGCAGCGACA 480
Qy 451 GACCCCACTCCAGTGTGGTGGTCCACGTCGTGAGAGTACCAGAGAGAAATGAGAGGAA 510
Db 481 GACACCACTCCAGTGTGGTGGTCCACGTCGTGAGAGTACCAGAGAGAAATGAGAGGAA 540
Qy 511 GAGGAAGAGATGGAGAGAAATGAAGAGAGACCCCAAGCCCAAAATCATCCAGACAGGAGACG 570
Db 541 GAGGAAGAGATGGAGAGAAATGAAGAGAGACCCCAAGCCCAAAATCATCCAGACAGGAGACG 600
Qy 571 GAGTACACACCGATCCACCTTAGCTGA 597
Db 601 GAGTACACACCGATCCACCTTAGCTGA 627

RESULT 8
BC013551 2198 bp mRNA linear ROD 07-AUG-2002
LOCUS Mus musculus, Down syndrome critical region homolog 1 (human),
DEFINITION clone MGC:19348 IMAGE:4236038, mRNA, complete cds.
ACCESSION BC013551
VERSION BC013551.1 GI:15488840
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg, R.
Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 25 Row: m Column: 6.
Location/Qualifiers
1. .2198
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
/clone="MGC:19348 IMAGE:4236038"
/tissue_type="kidney, normal, 5 month old male mouse."
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
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77. 673
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/db_xref="LocusID:54720"
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BASE COUNT 533 a 539 c 569 g 557 t
ORIGIN
Query Match 85.6%; Score 511; DB 10; Length 2198;
Best Local Similarity 93.8%; Pred. No. 1.2e-125;
Matches 532; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Qy 31 AGCGCCACCATCGCTGCCACCTGGACCGCGCTGTTCGTGGACGCGCTGCGGGGCC 90
Db 107 AGCTCCCTGATGCTTGTGTGGCAACGATGATGCTTCACGGAAGTGAGACACGAGGCC 166
Qy 91 AAATTTGAATCCCTCTTCAGAACATATGACAAGGACACACCTTCCAGTATTTTAAAGAGC 150
Db 167 AAATTTGAATCCCTCTTCAGAACATATGACAAGGACACACCTTCCAGTATTTTAAAGAGC 226
Qy 151 TTCAACGTTGTCGGATAACTTCAGCAACCCCTTATCTGACGCGGATGCCAGGCTGGG 210
Db 227 TTCAACGTTGTCGGATAACTTCAGCAACCCCTTATCTGACGCGGATGCCAGGCTGGG 286
Qy 211 CTGCACAGACCGAGTTCTCTGGGAAGAAATGAAGTTGTATTTTGTCTCAGACTTTACAC 270
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Qy 271 ATAGGAAGTTTACACACTGCTCCGCTCCGCAATCCGCAACAGTTCCTCATCTCCCTCCG 330
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Qy 331 GCCTCTCTCCCTGGCTGGAAACAAGTAGAAGATGCCACCCCGTCATAAATACGAT 390
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Qy 391 CTTTATATGCACTCTCAAGCTGGGCGCAGGAGAGATGATGAATGATGATGATGATGATGAT 450
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Qy 511 GAGGAAGAGATGGAGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCAGACAGGAGACCG 570
Db 587 GAGGAAGAGATGGAGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCAGACAGGAGACCG 646
Qy 571 GAGTACACACCGATCCACCTTAGCTGA 597
Db 647 GAGTACACACCGATCCACCTTAGCTGA 673

RESULT 9
AF263240 2224 bp mRNA linear ROD 30-MAY-2000
LOCUS Mus musculus calcineurin inhibitor mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF263240
VERSION AF263240.1 GI:8102013
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Fuentes, J.J., Pritchard, M.A., Pucharcos, C. and Estivill, X.
1 (bases 1 to 2224)
Down syndrome candidate region 1 (Dscr1), one of three
alternatively spliced exon 1 transcripts
Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 2224)
Fuentes, J.J., Pritchard, M.A., Pucharcos, C. and Estivill, X.
Direct Submission
TITLE
Submitted (02-MAY-2000) Centre de Genetica Medica i Molecular, IRO,
Avia, Castelldefels Km. 2.7, L'Hospitalet de Llobregat, Barcelona
08907, Spain
```

JOURNAL	Interacting protein (mclp) Patent: WO 0204491-A 14 17-JAN-2002; Board of Regents, The University of Texas System (US) ; Williams, Sanders R. (US) ; Rothermel, Beverly (US)	
FEATURES	Location/Qualifiers	
source	1..2212 /organism="Homo sapiens" /db_xref="taxon:9606" 25..618 /note="unnamed protein product" /codon_start=1 /protein_id="CAD23812.1" /translation="MEEVDLQDLPSATIACHLDPRFVDGLCRKAFESLFTFYDKDITD FOYFKSFRVIRNFNSPDSADARLQLKTEFLGKEMKLYFAQTLHIGSSHLAPPD KOFLLSPASPVPVGMKQVEDATPVINDLLYAIKSLGPGKEKVELHAATDTPVSVVH CESDOKEEEEEEMRRPKKIIQTRPEYPIHLS"	
CDS	BASE COUNT 588 a 455 c 529 g 640 t ORIGIN	
	Query Match 80.7%; Score 481.8; DB 6; Length 2212; Best Local Similarity 89.1%; Pred. No. 7.9e-118; Matches 532; Conservative 0; Mismatches 62; Indels 3; Gaps 1;	
	Qy 1 ATGGAGAGGTGGATCTGCAGGACCTGCCAGAGCGCCACCATCGCTGCCACCTGGACCCG 60	
	Db 25 ATGGAGAGGTGGACCTGCAGGACCTGCCAGCGCCACCATCGCTGCCACCTGGACCCG 84	
	Qy 61 CGCGTGTTCGTGACGGCCCTGTGCGGGCCCAATTTGAATCCCTCTTCAGACATATGAC 120	
	Db 85 CGCGTGTTCGTGACGGCCCTGTGCGGGCCCAATTTGAGTCCCTCTTTAGGACGTATGAC 144	
	Qy 121 AAGGACACCACTTCCAGTATTTAAGAGCTTCAAAAGCTGTCCGGATAAATTCAGCAAC 180	
	Db 145 AAGGACATACCTTTCAGTATTTAAGAGCTTCAAGAGTTCAGATAAATTCAGCAAC 204	
	Qy 181 CCCTTATTCGACGCGGATGCCAGGCTGCGGCTGCACAAGACCGAGTTCCTGGGGAAGAA 240	
	Db 205 CCCTTCTCCGACGAGATGCCAGGCTCCAGCTGCATAAGACTGAGTTTCTGGGAAAGAA 264	
	Qy 241 ATGAAGTTGTATTTTGTCTAGACTTTACACATAGGAGTTACACCTGGCTCGGCCAAT 300	
	Db 265 ATGAAGTTATATTTTGTCTAGACTTTACACATAGGAGCTACACCTGGCTCGGCCAAT 324	
	Qy 301 CCCACAAAACAGTTCCCTCATCTCCCTCCGCGCTCCTCCCTGCTGGTGGAAACAAGTA 360	
	Db 325 CCAGAACAGAGATTTCTGATCTCCCTCCGCGCTCCTCCGCGAGTGGATGGAAACAAGTG 384	
	Qy 361 GAAGATGCCACCCCGTCATAAATTTAGCATCTTTTATATGCCATCTCCAAGCTGGGGCCA 420	
	Db 385 GAAGATGGACCCAGTCATAAATATGATCTTATATGCCATCTCCAAGCTGGGGCCA 444	
	Qy 421 GGAGAGAGTATGAACCTGTCATGACGACAGACACCCACATCCCATGTGTGTGTCCAGTG 480	
	Db 445 GGGGAAAAGTATGAATTTGCACGACGACCTGACACCACTCCCAAGCTGGTGTGTCCATGA 504	
	Qy 481 TGTGAGAGTGCACCAAGAGATGAGGAGGAGAGAGAGATGAGAGATGAAGAGACCC 540	
	Db 505 TGTGAGAGTGCATCAAGAGGAGGAGAGAGAGAA---ATGGAAGATGAGGAGACCT 561	
	Qy 541 AAGCCCAAAATCATCCAGACCGGAGACCGGAGTACACACCGTACCACTTACCTGCA 597	
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RESULT 11	HSU85266 2227 bp mRNA linear PRI 19-APR-2000	
LOCUS	Homo sapiens down syndrome candidate region 1 (DSCR1) gene, alternative exon 1, complete cds.	
DEFINITION	Homo sapiens down syndrome candidate region 1 (DSCR1) gene, alternative exon 1, complete cds.	
ACCESSION	U85266	
VERSION	U85266.2	
KEYWORDS	GI:7596913	



[illegible]



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BASE COUNT 628 a 465 c 555 g 641 t
ORIGIN
Query Match 80.7%; Score 481.8; DB 9; Length 2289;
Best Local Similarity 89.1%; Pred. No. 7.9e-118;
Matches 532; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 ATGGAGGAGGTGGATCTGCAGGACCTGCCGAGCGCCACCATCGCCTGCCACCTGGACCCG 60
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QY 61 CCGCTGTTCTGGACGGCTGTGCCGGGCAAAATTGAATCCCTTTCAGACATATGAC 120
DB 126 CCGCTGTTCTGGACGGCTGTGCCGGGCAAAATTGAATCCCTTTCAGACATATGAC 185
QY 121 AAGGACACACCTTCCAGTATTTAAAGAGCTTCAACAGTGTCCGGATAAATTCAGCAAC 180
DB 186 AAGGACATCACCTTTCAGTATTTAAAGAGCTTCAACAGTGTCCGGATAAATTCAGCAAC 245
QY 181 CCTTATCTGCAGCGATGCCAGGTGTCCGGGTGCACAGACCGAGTTCCTGGGGAAGAA 240
DB 246 CCTTCTCCGACGACAGTCCAGGCTCCAGCTGCATAGAGCTCAGTTTCTGGGAAGAA 305
QY 241 ATGAAGTTCTATTGTCTCAGACTTTACACATAGGAAGTTCACACCTGCTCCGCCAAT 300
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DB 366 CCAGACAAGCAGTCTTGTATCTCCCTCCGCTCTCCGCGAGTGGGATGGAAACAAGTG 425
QY 361 GAAGATGCCACCCCGTCAATAATTAGGATCTTTATATGCCATCTCCAAAGCTGGGGCCA 420
DB 426 GAAGATGCCACCCCGTCAATAACTATGATCTCTTATATGCCATCTCCAAAGCTGGGGCCA 485
QY 421 GGAGAGAAGTATGAAGTGCATGCAGCAGCAGACCCACCTCCAGTGTGGTCCACGTG 480
DB 486 GGGGAAAGATGAATGTGACGCGAGTGCACACCTCCAGCGGTGGTGTCCATGTA 545
QY 481 TGTGAGTGCACCAAGAGAAATGAGGAGGAGAGAGAGATGAGAGAAATGAAGACACC 540
DB 546 TGTGAGTGCATCAGAGAGAGGAGAGAGAGAGAA--ATGGAAGATGAGGACACCT 602
QY 541 AAGCCCAAAATCATCCAGACACGGAGACCGGAGTACACACCGATCCACCTTACGCTGA 597
DB 603 AAGCCCAAAATCATCCAGACACGGAGACCGGAGTACACACCGATCCACCTCAGCTGA 659

RESULT 13
AK092184
LOCUS
DEFINITION
Homo sapiens cDNA FLJ34865 fis, clone NT2NE2014104, highly similar
to DOWN SYNDROME CRITICAL REGION PROTEIN 1.
ACCESSION
AK092184
VERSION
AK092184.1 GI:21750714
KEYWORDS
oligo capping; fls (full insert sequence).

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clone_lib:NT2NE2 clone:NT2NE2014104.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuwa,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Murakawa,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Sugiyama,A., Kawakami,B., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2407)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'-6 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
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/clone="NT2NE2014104"
/cell_line="NT2"
/clone_lib="NT2NE2"
/notes="cloning vector: pME18SL3-mRNA from NT2 neuron
after the differentiation of NT2 neuronal precursor
cells."
BASE COUNT 607 a 519 c 627 g 654 t
ORIGIN
Query Match 80.7%; Score 481.8; DB 9; Length 2407;
Best Local Similarity 89.1%; Pred. No. 7.9e-118;
Matches 532; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 ATGGAGGAGGTGGATCTGCAGGACCTGCCGAGCGCCACCATCGCCTGCCACCTGGACCCG 60
DB 218 ATGGAGGAGGTGGACCTGCAGGACCTGCCGAGCGCCACCATCGCCTGTCTACCTGGACCCG 277
QY 61 CCGCTGTTCTGGACGGCTGTGCCGGGCAAAATTTGAATCCCTTTCAGAACATATGAC 120
DB 278 CCGCTGTTCTGGACGGCTGTGCCGGGCAAAATTTGAGTCCCTTTTAGAGCTATGAC 337
QY 121 AAGGACACACCTTCCAGTATTTTAAGAGCTTCAACAGTGTCCGAGTAAATCTTCAGCAAC 180
DB 338 AAGGACATCACCTTTCAGTATTTTAAGAGCTTCAACAGTGTCCAGAGTCAAGAACTTCAGCAAC 397
QY 181 CCCTTATCTGCAGCGATGCCAGGCTGCCGCTGCACAAAGACCGAGTTCCTGGGGAAGAA 240
DB 398 CCCTTCTCCGACGACATGCCAGCTCCAGCTGCATTAAGACTGAGTTTCTGGGAAAGAA 457
QY 241 ATGAAGTTGATTTTGTCTCAGACTTTACACATAGGAAGTTCACACCTGGCTCCGCCCAAT 300
DB 458 ATGAAGTTTATTTTGTCTCAGACTTTACACATAGGAAGTTCACACCTGGCTCCGCCCAAT 517
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QY 361 GAAGATGCCACCCCGTCATAAAATTAGCATCTTTATATGCCATCTCCAAAGCTGGGGCCA 420
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RESULT 14
AB075973 626 bp mRNA linear ROD 27-JUL-2002
LOCUS
DEFINITION
Rattus norvegicus mcip 1 mRNA for myocyte-enriched
calcineurin-interacting protein 1, complete cds.
ACCESSION
AB075973
VERSION
AB075973.1 GI:21998843
KEYWORDS
SOURCE
Rattus norvegicus cDNA to mRNA..
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 Odashima,M., Nagata,K., Obata,K., Somura,F., Izawa,H., Miyazaki,T.,
Murata,Y., Seo,H., Yamada,Y. and Yokota,M.
rat myocyte-enriched calcineurin interactin protein 1, splice
variant 4 mRNA, complete cds
Unpublished
REFERENCE
2 (bases 1 to 626)
Obata,K., Nagata,K., Odashima,M., Somura,F., Yamada,Y. and
Yokota,M.
Direct Submission
Submitted (11-DEC-2001) Koji Obata, Nagoya University, Department
of Clinical Pathophysiology; 65 Tsurumai-cho, Showa-ku, Nagoya,
Aichi 466-8550, Japan (E-mail:obata@etsu.med.nagoya-u.ac.jp,
Tel:81-52-744-2577, Fax:81-52-744-2977)
FEATURES
Location/Qualifiers
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BASE COUNT 182 a 163 c 154 g 127 t
ORIGIN
Query Match 72.28; Score 430.8; DB 10; Length 626;
Best Local Similarity 86.08; Pred. No. 2.9e-104;
Matches 490; Conservative 0; Mismatches 77; Indels 3; Gaps 1;
QY 31 AGCGCCACATCGCTGCCACCTGGACCGCGCTGTTCGTGGACGGCGCTGCGCGGCC 90
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QY 151 TTCAACAGCTGTCGGGATAACTTTCAGCAACCCCTTATCTGCAGCCGATGCAGGCTGCGG 210
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QY 331 GCCTCTCTCCCTGCTGCTGGAACAAGTAGAAGATGCCACCCCGCTATAAAATTTACGAT 390
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QY 391 CTTTATATGCCATCTCCAAAGCTGGGCCAGGAGAGAAAGTATGAACATGTCAGCGGACA 450
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QY 451 GACCCCACTCCCACTGTCGTCCTCCAGCTGTGTGAGAGTACCAAGAGATGAGGAGGAA 510
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QY 568 CCGGAGTACACACCGATCCACCTTAGCTGA 597
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RESULT 15
CGU60263 2216 bp mRNA linear ROD 03-SEP-1997
LOCUS
DEFINITION
Cricetulus griseus Adapt78 (adapt78) mRNA, complete cds.
ACCESSION
U60263
VERSION
U60263.1 GI:2351390
KEYWORDS
Cricetulus griseus.
Cricetulus griseus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Cricetulus.
REFERENCE
1 (bases 1 to 2216)
Crawford,D.R., Leahy,K.P., Abramova,N., Lan,L., Wang,Y. and
Davies,K.J.
Hamster adapt78 mRNA is a Down syndrome critical region homologue
that is inducible by oxidative stress
JOURNAL
Arch. Biochem. Biophys. 342 (1), 6-12 (1997)
MEDLINE
97329095
PUBMED
9185608
REFERENCE
2 (bases 1 to 2216)
Crawford,D.R., Leahy,K.L. and Davies,K.J.A.
Direct Submission
TITLE
Submitted (10-JUN-1996) Biochem. and Mol. Biol., Albany Medical
College, 47 New Scotland Avenue, Albany, NY 12208, USA
JOURNAL
Location/Qualifiers
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/cell_type="HA-1"
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70..663
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calcium-inducible mRNA"
/codon_start=1
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BASE COUNT 544 a 515 c 564 g 593 t  
ORIGIN

Query Match		71.7%;	Score 427.8;	DB 10;	Length 2216;
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				Indels	3;
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QY	211	CTGCACAAGACCGAGTTCCTGGGGAAGGAAATGAAGTTGTATTTTGTCTCAGACTTTACAC	270		
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QY	391	CTTTTATATGCCATCTCCAAGCTGGGCCAGGAGAGAAATGAACTGATGCGAGGACA	450		
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QY	451	GACCCCACTCCAGTGTGGTGTCCAGCTGTGTGAGAGTGACCAAGAGATGAGGAGAA	510		
Db	520	GACCCCACTCCAGTGTGGTGTCCAGCTGTGTGAGAGTGACCAAGAGATGAGGAGAA	576		
QY	511	GAGGAAGAGATGGAGAGATGAAGACACCAAGCCCAAAATCATCCAGACCGAGACCG	570		
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Copyright (c) 1993 - 2002 CompuGen Ltd.

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9958.837 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	597	100.0	597	24	Human MCIP associa
2	515.8	86.4	597	24	Mouse MCIP associa
3	481.8	80.7	2212	24	Human MCIP associa
4	469	78.6	2358	21	Lung cancer associ
5	426.2	71.4	599	24	Human MCIP associa
6	403.8	67.6	2331	24	Human MCIP associa
7	399.6	66.9	2173	24	Gene #3341 used to
8	398	66.7	2174	20	Human DSCR1 coding
9	392.8	65.8	2348	20	Human DNA sequence

10	211	35.3	934	22	AAF25338	Nucleotide sequenc
11	211	35.3	3159	24	AA911457	Human Down syndrom
12	207	34.7	442	21	AA011774	Human secreted pro
13	193	32.3	3184	24	AA030157	Human MCIP associa
14	193	32.3	3184	24	ABL61768	Colon adenocarcino
15	193	32.3	3184	24	ABL65187	Lung cancer relate
16	186.4	31.2	720	24	AA030159	Human MCIP associa
17	186.4	31.2	828	24	AA030158	Human MCIP associa
18	184.6	30.9	615	24	ABA91463	Rat Down syndrome
19	183	30.7	594	24	AA030154	Mouse MCIP associa
20	144.6	24.2	412	22	ABA56172	Human foetal liver
21	144.6	24.2	412	22	AAK04364	Human brain expres
22	144.6	24.2	412	22	AAI14449	Probe #4382 for ge
23	144.6	24.2	412	22	AAI35821	Probe #4507 used t
24	144.6	24.2	412	22	AAI04272	Probe #4263 used t
25	144.6	24.2	412	24	ABS04419	Human genome-deriv
26	144.6	24.2	446	22	ABA43406	Human breast cell
27	144.6	24.2	446	22	ABA53852	Human foetal liver
28	144.6	24.2	446	22	ABA23398	Probe #2064 for ge
29	144.6	24.2	446	22	AAK02113	Human brain expres
30	144.6	24.2	446	22	AAK27563	Human bone marrow
31	144.6	24.2	446	22	AAI12148	Probe #2081 for ge
32	144.6	24.2	446	22	AAI33493	Probe #2179 used t
33	144.6	24.2	446	22	AAI02061	Probe #2052 used t
34	144.6	24.2	446	24	ABS02041	Human genome-deriv
35	136.6	22.9	1021	24	ABA91458	Rat Down syndrome
36	123	20.6	486	22	ABA42132	Human breast cell
37	123	20.6	486	22	ABA52554	Human foetal liver
38	123	20.6	486	22	ABA22343	Probe #809 for gen
39	123	20.6	486	22	AAK00816	Human brain expres
40	123	20.6	486	22	AAK26270	Human bone marrow
41	123	20.6	486	22	AAI10903	Probe #836 for gen
42	123	20.6	486	22	AAI32163	Probe #849 used to
43	123	20.6	486	22	AAI00825	Probe #816 used to
44	123	20.6	486	24	ABS00858	Human genome-deriv
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ALIGNMENTS

RESULT 1  
AAD30152  
ID AAD30152 standard; DNA; 597 BP.  
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AC AAD30152;  
XX  
DT 17-MAY-2002 (first entry)  
DE Human MCIP associated DNA #2.  
XX  
KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;  
KW heart failure; cardiomyopathy; heart disease; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key  
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FT /\*tag= a  
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XX WO200204491-A2.  
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PD 17-JAN-2002.  
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PF 06-JUL-2001; 2001WO-US21662.  
XX  
PR 07-JUL-2000; 2000US-216601P.  
XX  
PR 13-FEB-2001; 2001US-0782953.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (WILL/) WILLIAMS S R.  
PA (ROTH/) ROTHERMEL B.

XX Williams SR, Rothermel B;  
XX WPT: 2002-179698/23.  
DR P-PSDB; AAE18911.  
XX  
XX Screening for modulators of muscle calcineurin interacting protein  
PT (MCIP) binding, expression or phosphorylation, useful for treating  
PT cardiac hypertrophy or heart failure, comprises mixing MCIP,  
PT calcineurin and a test compound -  
XX  
XX Claim 95; Page 147-148; 174pp; English.  
XX  
XX The invention relates to muscle calcineurin interacting proteins (MCIPs)  
CC and nucleic acid molecules encoding such proteins. MCIPs form a physical  
CC complex with the catalytic subunit of calcineurin and increased levels  
CC of MCIPs correspond to a reduced ability of calcineurin to stimulate  
CC transduction of certain target genes. The invention also relates to  
CC methods for identifying modulators of MCIP binding, expression or  
CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin  
CC may be used for treating cardiac hypertrophy and heart failure.  
CC Antibodies to MCIP can be used in characterising the MCIP content of  
CC healthy and diseased tissues and subsequently for determining the  
CC presence or absence of cardiomyopathy or as predictor of heart disease.  
CC The present sequence is human MCIP associated DNA.  
XX  
XX Sequence 597 BP; 160 A; 170 C; 151 G; 116 T; 0 other;  
SQ  
Query Match 100.0%; Score 597; DB 24; Length 597;  
Best Local Similarity 100.0%; Pred. No. 1.1e-169;  
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 ATGGAGGAGTGGATCGAGCACTGCGGAGCGCCACCATCGCTGCACCTGGACCCG 60  
QY 61 CGCTGCTGCTGACGGCTGTGCGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 120  
DB 61 CGCTGCTGCTGACGGCTGTGCGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 120  
QY 121 AAGGACACCACTTCCAGTATTTAGAGCTTCAACGCTCCGATTAACCTTCAGCAAC 180  
DB 121 AAGGACACCACTTCCAGTATTTAGAGCTTCAACGCTCCGATTAACCTTCAGCAAC 180  
QY 181 CCCTATCTCAGCCGATGCGGCTGCGCTGCACAGACCGAGTTCCTGGGGAAGGAA 240  
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QY 301 CCCGACAAACAGTTCCTCATCTCCCTCGGCTCTCTCCCTGGCTGGAAACAGTA 360  
DB 301 CCCGACAAACAGTTCCTCATCTCCCTCGGCTCTCTCCCTGGCTGGAAACAGTA 360  
QY 361 GAAGATGCCACCCCGCTCAATAATTTAGATCTTTTATGCCATCTCCAGCTGGGGCCA 420  
DB 361 GAAGATGCCACCCCGCTCAATAATTTAGATCTTTTATGCCATCTCCAGCTGGGGCCA 420  
QY 421 GGAGAGAAGTATGAATGCTATGACGAGACAGACCCCACTCCAGTGTGGTCCACGTG 480  
DB 421 GGAGAGAAGTATGAATGCTATGACGAGACAGACCCCACTCCAGTGTGGTCCACGTG 480  
QY 481 TGTGAGAGTACCAAGAGATGAGGAGGAAGAGAGATGGAGAGATGAAGAGACCC 540  
DB 481 TGTGAGAGTACCAAGAGATGAGGAGGAAGAGAGATGGAGAGATGAAGAGACCC 540  
QY 541 AAGCCCAAAATCATCCAGACACGAGACCGGAGTACACACCGATCCACCTTAGCTGA 597  
DB 541 AAGCCCAAAATCATCCAGACACGAGACCGGAGTACACACCGATCCACCTTAGCTGA 597

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AAD30153 standard; DNA; 597 BP.  
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XX AAD30153;  
XX  
XX 17-MAY-2002 (first entry)  
XX Mouse MCIP associated DNA #3.  
XX Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;  
KW heart failure; cardiomyopathy; heart disease; mouse; gene; ds.  
XX  
XX Mus musculus.  
XX  
XX Location/Qualifiers  
FH Key 1..597  
FT CDS /tag- a  
FT /product= "Mouse MCIP associated protein #3"  
XX  
XX WO200204491-A2.  
XX  
XX 17-JAN-2002.  
XX  
XX 06-JUL-2001; 2001WO-US21662.  
XX  
XX 07-JUL-2000; 2000US-216601P.  
XX 13-FEB-2001; 2001US-0782953.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA (WILL/) WILLIAMS S R.  
PA (ROTH/) ROTHERMEL B.  
XX  
XX Williams SR, Rothermel B;  
PI  
XX  
XX WPT: 2002-179698/23.  
DR P-PSDB; AAE18912.  
XX  
XX Screening for modulators of muscle calcineurin interacting protein  
PT (MCIP) binding, expression or phosphorylation, useful for treating  
PT cardiac hypertrophy or heart failure, comprises mixing MCIP,  
PT calcineurin and a test compound -  
XX  
XX  
XX Disclosure; Page 150-151; 174pp; English.  
XX  
XX The invention relates to muscle calcineurin interacting proteins (MCIPs)  
CC and nucleic acid molecules encoding such proteins. MCIPs form a physical  
CC complex with the catalytic subunit of calcineurin and increased levels  
CC of MCIPs correspond to a reduced ability of calcineurin to stimulate  
CC transduction of certain target genes. The invention also relates to  
CC methods for identifying modulators of MCIP binding, expression or  
CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin  
CC may be used for treating cardiac hypertrophy and heart failure.  
CC Antibodies to MCIP can be used in characterising the MCIP content of  
CC healthy and diseased tissues and subsequently for determining the  
CC presence or absence of cardiomyopathy or as predictor of heart disease.  
CC The present sequence is mouse MCIP associated DNA.  
CC Note: This sequence has been described as human MCIP3 encoding DNA  
CC in the specification, however the sequence seems to be a polynucleotide  
CC encoding a MCIP associated protein.  
XX  
XX Sequence 597 BP; 170 A; 156 C; 142 G; 129 T; 0 other;  
SQ  
Query Match 86.4%; Score 515.8; DB 24; Length 597;  
Best Local Similarity 94.4%; Pred. No. 3.3e-145;  
Matches 535; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 31 AGCGCACCATCGCTGCCACCTGGACCCGCGCTGTTCTGGAGCGCTGTGCGGGGCC 90  
DB 31 AGCTCCCTGATGCTTGTGTGGCAACGATGATGCTTTCAGCGAAAGTGAGACAGGCC 90  
QY 91 AAATTGATCCCTCTTCAGACATATGACAGGACACCCCTCCAGTATTTTAAGAGC 150

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QY	151	TTCAAAACGTGTCGGATAAACATTCAACACCCCTTATCTGCAGCCGATGCCAGGCTCGGG	210
Db	151	TTCAAAACGTGTCGGATAAACATTCAACACCCCTTATCTGCAGCCGATGCCAGGCTCGGG	210
QY	211	CTGCACAAGACCGAGTTCCTCGGGGAGGAAATCAAGTCTGATTCTTCAGACTTTACAC	270
Db	211	CTGCACAAGACCGAGTTCCTCGGGGAGGAAATGAAGTGTATTTTGTCTCAGACTTTTACAC	270
QY	271	ATAGGAAGTTCAACACTTGGCTCCGCCCAATCCGCACAAACAGTTCTCATCTCCCTCCG	330
Db	271	ATAGGAAGTTCAACACTTGGCTCCGCCCAATCCGCACAAACAGTTCTCATCTCCCTCCG	330
QY	331	GCCTCTCTCCCGTTGGCTGGAAACAAGTAGAAGATGCCACCCCGTCTATAAATTACGAT	390
Db	331	GCCTCTCTCCCGTTGGCTGGAAACAAGTAGAAGATGCCACCCCGTCTATAAATTACGAT	390
QY	391	CTTTTATATGCCATCTCCAAGCTGGGGCCAGAGAGAGAAGTATGAATCGCATCGACGACA	450
Db	391	CTTTTATATGCCATCTCCAAGCTGGGGCCAGAGAGAGAAGTATGAATCGCATCGACGACA	450
QY	451	GACCCCACTCCCAAGTGTGGTGTCACGTGTGTGAGAGTGAACAAGAGAAATGAGGAGGAA	510
Db	451	GACCCCACTCCCAAGTGTGGTGTCACGTGTGTGAGAGTGAACAAGAGAAATGAGGAGGAA	510
QY	511	GAGGAAGAGATGGAGAGAATGAAGACACCCAGCCCCAAAATCATCCAGACCGGAGACCG	570
Db	511	GAGGAAGAGATGGAGAGAATGAAGACACCCAGCCCCAAAATCATCCAGACCGGAGACCG	570
QY	571	GAGTACACACCGATCCACCTTAGCTGA	597
Db	571	GAGTACACACCGATCCACCTTAGCTGA	597

RESULT 3	
AAD30156	
ID	AAD30156 standard; DNA; 2212 BP.
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XX	AAD30156;
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XX	17-MAY-2002 (first entry)
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XX	Human MCIP associated DNA #2.
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XX	
XX	Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
KW	heart failure; cardiomyopathy; heart disease; human; gene; ds.
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OS	Homo sapiens.
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XX	17-JAN-2002.
XX	
XX	06-JUL-2001; 2001WO-US21662.
XX	
XX	07-JUL-2000; 2000US-216601P.
PR	
PR	13-FEB-2001; 2001US-0782953.
XX	
XX	(TEXA ) UNIV TEXAS SYSTEM.
PA	(WILL/) WILLIAMS S R.
PA	(ROTH/) ROTHERMEL B.
XX	
PI	Williams SR, Rothermel B;
XX	
XX	WPI; 2002-179698/23.
DR	P-PSDB; AAE18915.
XX	

PT	Screening for modulators of muscle calcineurin interacting protein
PT	(MCIP) binding, expression or phosphorylation, useful for treating
PT	cardiac hypertrophy or heart failure, comprises mixing MCIP,
PT	calcineurin and a test compound -
XX	
PS	Example 1; Page 159-161; 174pp; English.
XX	
CC	The invention relates to muscle calcineurin interacting proteins (MCIPs)
CC	and nucleic acid molecules encoding such proteins. MCIPs form a physical
CC	complex with the catalytic subunit of calcineurin and increased levels
CC	of MCIPs correspond to a reduced ability of calcineurin to stimulate
CC	transcription of certain target genes. The invention also relates to
CC	methods for identifying modulators of MCIP binding, expression or
CC	phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
CC	may be used for treating cardiac hypertrophy and heart failure.
CC	Antibodies to MCIP can be used in characterising the MCIP content of
CC	healthy and diseased tissues and subsequently for determining the
CC	presence or absence of cardiomyopathy or as predictor of heart disease.
CC	The present sequence is human MCIP associated DNA.
CC	Note: This sequence has been described as murine MCIP splice variant in
CC	the specification, however the sequence seems to be a polynucleotide
CC	encoding a MCIP associated protein.
XX	
SQ	Sequence 2212 BP; 588 A; 455 C; 529 G; 640 T; 0 other;
	Query Match            80.7%; Score 481.8; DB 24; Length 2212;
PT	Best Local Similarity    89.1%; Pred. No. 1.1e-134;
MT	Matches 532; Conservative    0; Mismatches 52; Indels    3; Gaps    1;
QY	1 ATGGAGGAGGTGGATCTCGAGGACCTCCGAGCGCCACCATCGCCTGCCACTTGACCCG 60
DB	
DY	25 ATGGAGGAGGTGGACCTTCGAGGACCTGCCAGCGCCACCATTGGCTGTCACCTGGACCCG 84
QY	61 CGCGTGTTCGTGGACGCCTGTGCGGGGCCAAATTTGAATCCCCTCTTCAGAACATATGAC 120
DB	
DY	85 CGCGTGTTCGTGGACGCCTGTGCGGGGCCAAATTTGAGTCCCTCTTTAGACCATATGAC 144
QY	121 AAGGACACCACTTCCAGTAGTATTTTAAGAGCTTCAAACTGTCCGATATAAATCTTCAGCAAC 180
DB	
DY	145 AAGGACATCACCTTTCAGTAGTATTTTAAGAGCTTCAACAGAGTCAGANATAAATCTTCAGCAAC 204
QY	181 CCCATTATCTCGACCGCATGCCAGCTCGCGCTGCACAAGACCGAGTTCCTGGGGAAGGAA 240
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DY	205 CCCTTCTCCGACGAGATGCCAGGCTCCAGCTGCATTAAGACTGAGTTTCTGGGAAAGGAA 264
QY	241 ATGAAGTGTATTTTGTCTCAGACTTTACATAGAAGTAGTTCACACCTGGCTCCGCCCAAT 300
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DY	265 ATGAAGTGTATTTTGTCTCAGACCTTACATAGTAGAGCTCACACCTGGCTCCGCCCAAT 324
QY	301 CCGACAAAAGTTCCTCATCTCCCTCCGSCCTCTCCTCCGPTGTGCTGAAACAAGTA 360
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DY	325 CCAGCAAGCAGATTCTTGATCTCCCTTCGCGCTCTCCGCGAGTGGATGAAACAAGTG 384
QY	361 GAAGATGCCACCCCGTCATAAATATGAGATCTTTTATATGCCATCTCCAAGCTGGGGCCA 420
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DY	385 GAAGATCGGACCCAGTCATAAATATGATCTTATATGCCATCTCAAAGCTGGGGCCA 444
QY	421 GGAGAGAAGTATGAATTCGATGACAGCAGACACCCCACTCCCAAGTGTGGTCCACGTG 480
DB	
DY	445 GGGGAAAAGTATGAATTTGCAGCGACGACACTGACACCACTCCCAAGCTGGTGCATGTA 504
QY	481 TGTCAGATGTACCAAGAGAATGAGGAGGAAGAGCAAGATGGAGAGAAATGAACAGACCC 540
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DY	505 TGTGAGATGTATCAAGAGAGGAGGAAGAGAGGAA ---ATGGAAAGAATGAGGAGACCT 561
QY	541 AAGCCCCAAATCATCCAGACACGGAGACCGGAGTACACACCGATCCACCTTAGCTGA 597
DB	
DY	562 AAGCCAAATTTATCCAGACACGAGGCGGAGTACACGCGGATCCACCTCAGCTGA 618
AD	
RESULT 4	
AAF18328	
DN	AAF1R328 standard. DNA: 2158 BP





transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure. Antibodies to MCIP can be used in characterizing the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease. The present sequence is human MCIP associated DNA.

Sequence 599 BP; 164 A; 150 C; 149 G; 136 T; 0 other;

Query Match 71.4%; Score 426.2; DB 24; Length 599;  
Best Local Similarity 93.1%; Pred. No. 3.4e-118;  
Matches 457; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 31 AGCGCCACACCGCTGCGCCACCTGCGCCGCGCTGCTGCGACGCGCTGCGCGGCC 90  
DB 110 AGCTCCCTGATGCTGTGGCAACGATGATGCTTCAGCGAAGTGAGACCGGCC 169  
QY 91 AAATTTGAATCCCTCTCAGAACATATGACAAGGACACACCTTCCAGTATTTAAGAGC 150  
DB 170 AAATTTGAATCCCTCTCAGAACATATGACAAGGACACACCTTCCAGTATTTAAGAGC 229  
QY 151 TTCAAACGTGCGGATTAACCTTACGACACCCCTTATCTGCGAGCGATGCCAGGCTGCGG 210  
DB 230 TTCAAACGTGCGGATTAACCTTACGACACCCCTTATCTGCGAGCGATGCCAGGCTGCGG 289  
QY 211 CTGCAACAGACCGAGTCTCTGCGGGAAGAAATGAAGTTGATTTGCTCAGACTTTACAC 270  
DB 290 CTGCAACAGACCGAGTCTCTGCGGGAAGAAATGAAGTTGATTTGCTCAGACTTTACAC 349  
QY 271 ATAGGAAGTTACACCTGCTCGGCCCAATCCGCAACAGTTCTCATCTCCCTCGG 330  
DB 350 ATAGGAAGTTACACCTGCTCGGCCCAATCCGCAACAGTTCTCATCTCCCTCGG 408  
QY 331 GCCTCTCTCCGTTGGTGGGAACAGTAGAAGATGCCACCCCGTCAATAAATACGAT 390  
DB 409 GCCTCTCTCCGTTGGTGGGAACAGTAGAAGATGCCACCCCGTCAATAAATACGAT 468  
QY 391 CTTTATATGTCATCTCCAAGCTGGGCGCAGGAGAGATGAACTGCATGCAGCGACA 450  
DB 469 CTTTATATGTCATCTCCAAGCTGGGCGCAGGAGAGATGAACTGCATGCAGCGACA 528  
QY 451 GACCCCACTCCAGTGTGGTGTCCACGCTGTGTGAGAGTGACCAAGAGATGAGGAGAA 510  
DB 529 GACACCACTCCAGTGTGGTGTCCACGCTGTGTGAGAGTGACCAAGAGATGAGGAGAA 588  
QY 511 GAGGAAGAGAT 521  
DB 589 GAGGAAGAGAT 599

## RESULT 6

AAD30155

ID AAD30155 standard; DNA; 2331 BP.

XX AC AAD30155;

XX DT 17-MAY-2002 (first entry)

XX DE Human MCIP associated DNA #1.

XX KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;

XX KW heart failure; cardiomyopathy; heart disease; human; gene; ds.

XX OS Homo sapiens.

XX FH Key

XX FT 144..737

XX FT CDS

XX FT /\*tag=

XX FT /product= "Human MCIP associated protein #1"

XX PN WO200204491-A2.

XX 17-JAN-2002.  
XX 06-JUL-2001; 2001WO-US21662.  
XX 07-JUL-2000; 2000US-216601P.  
XX 13-FEB-2001; 2001US-0782953.  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX (WILL/) WILLIAMS S R.  
XX (ROTH/) ROTHERMEL B.  
XX Williams SR, Rothermel B;  
XX WPI; 2002-179698/23.  
XX P-PSDB; AAE18914.  
XX Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound -  
XX Claim 72; Page 155-157; 174pp; English.  
XX The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure.  
XX Antibodies to MCIP can be used in characterizing the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease.  
XX The present sequence is human MCIP associated DNA.  
XX Note: This sequence has been described as a promoter in claim 72 of the specification, however the sequence seems to be a polynucleotide encoding a MCIP associated protein.  
XX SQ Sequence 2331 BP; 630 A; 470 C; 547 G; 684 T; 0 other;

Query Match 67.6%; Score 403.8; DB 24; Length 2331;  
Best Local Similarity 83.2%; Pred. No. 3.7e-111;  
Matches 472; Conservative 0; Mismatches 92; Indels 3; Gaps 1;  
QY 31 AGCGCCACACCGCTGCGCCACCTGCGCCGCGCTGCTGCGACGCGCTGCGCGGCC 90  
DB 174 AGCTCCCTGATGCTGCTGCGCAACAGTATATCTTCAGCGAAGTGAACCGAGGCC 233  
QY 91 AAATTTGAATCCCTCTTCAGAACATATGACAAGGACACACCTTCCAGTATTTAAGAGC 150  
DB 234 AAATTTGAGTCCCTCTTTAGGAGCTATGACAAGGACATCACCTTTTCAGTATTTAAGAGC 293  
QY 151 TTCAAACGTGTCGGGATAAAGTTCAGCAACCCCTTATCTGCGACCGATGCCAGGCTGCGG 210  
DB 294 TTCAAACGAGTCAAGATAAAGTTCAGCAACCCCTTCTCCGCGACAGATGCCAGGCTCCAG 353  
QY 211 CTGCAACAGCCAGTTCCTGCGGGAAGAAATGAAGTTGATTTGCTCAGACTTTACAC 270  
DB 354 CTGCATTAAGCTGAGTTTCTGGGAAAGAAATGAAGTTATATTTGCTCAGACTTTACAC 413  
QY 271 ATAGGAAGTTACACCTGCTCGGCCCAATCCGCAACAGATTCCTCATCTCCCTCGG 330  
DB 414 ATAGGAAGTCTCACCTGCTCGGCCCAATCCGCAACAGATTTCTGATCTCCCTCCG 473  
QY 331 GCCTCTCTCCGTTGGTGGGAACAGTAGAAGATGCCACCCCGTCAATAAATACGAT 390  
DB 474 GCCTCTCCGCGAGTGGGATGGAACCAAGTGAAGATGCCACCCCGTCAATAAATACGAT 533  
QY 391 CTTTATATGTCATCTCCAAGCTGGGCGCAGGAGAGATGAACTGCATGCAGCGACA 450  
DB 534 CTCTTATATGCCATCTCCAAGCTGGGCGCAGGAGAGATGAACTGCATGCAGCGAGCT 599

451 GACCCCTCCAGTGTGGTCCACGCTGTGAGAGTGACCAAGAGAGATGAGGAGAA 510  
Db 594 GACACCACTCCAGCGTGGTGGTCCATGTATGTGAGAGTGATCAAGAGAGGAGGAGAA 653  
Qy 511 GAGGAAGAGATGGAGAGAAATCAAGAGACCAAGCCCAAAATATCCAGACACGAGACCG 570  
Db 654 GAGGAA---ATGGAAGAAGATGAGAGACCTTAAGCCAAATATCCAGACGAGGAGCCG 710  
Qy 571 GAGTACACACCGATCCACCTTAGCTGA 597  
Db 711 GAGTACACGCGGATCCACCTCAGCTGA 737

RESULT 7  
ABN96843  
ID ABN96843 standard; DNA; 2173 BP.  
AC ABN96843;  
XX  
DT 13-AUG-2002 (first entry)  
DE Gene #3341 used to diagnose liver cancer.  
XX  
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;  
KW metastatic liver tumour; cytostatic; expression profile; disease state;  
KW disease progression; drug toxicity; drug efficacy; drug metabolism.  
XX  
OS Homo sapiens.  
XX  
PN WO200229103-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 02-OCT-2001; 2001WO-US30589.  
XX  
PR 02-OCT-2000; 2000US-237054P.  
XX  
PA (GENE-) GENE LOGIC INC.  
XX  
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;  
XX  
DR WPI; 2002-426119/45.  
XX  
PT Diagnosing and detecting the progression of liver cancer,  
PT hepatocellular carcinoma or metastatic liver tumor in a patient,  
PT involves detecting the level of expression of two or more genes in a  
PT liver tissue sample -  
XX  
PS Claim 1; SEQ ID NO 3341; 298pp; English.  
XX  
CC The invention relates to a novel method for diagnosing and detecting the  
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver  
CC tumour in a patient, and differentiating metastatic liver cancer from  
CC hepatocellular carcinoma in a patient, involving detecting the level of  
CC expression of two or more genes represented in ABN93503-ABN97455 in a  
CC tissue sample. The method of the invention has hepatotropic, and  
CC cytostatic activity. The method is useful for diagnosing and detecting  
CC the progression of liver cancer, hepatocellular carcinoma and metastatic  
CC liver carcinoma in a patient. The method is useful for identifying  
CC expression profiles which serve as useful diagnostic markers as well as  
CC markers that can be used to monitor disease states, disease progression,  
CC drug toxicity, drug efficacy and drug metabolism.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 2173 BP; 606 A; 431 C; 503 G; 633 T; 0 other;

Query Match 66.9%; Score 399.6; DB 24; Length 2173;  
Best Local Similarity 87.8%; Pred. No. 6.6e-110;  
Matches 448; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

Qy 88 GCCAAATTTGAATCCCTCTTCAGAACATATGACAAGACACACCCTTCCAGTATTTAAG 147  
Db 58 GCCAAATTTGAGTCCCTCTTTAGGACGTATGACAAGACATCACCTTTTCAGTATTTAAG 117  
Qy 148 AGCTTCAACCTGTCGGATAACTTCAAGCAACCCCTTATCTGCAGCCGATGCCAGGCTG 207  
Db 118 AGCTTCAACCTGTCAGATTAACCTTCAAGCAACCCCTTCTCCGACGAGATGCCAGGCTC 177  
Qy 208 CGGCTGCACAAGACCGAGTTCTCTGGGGAAGAAATGAAGTTGTATTTTGTCTCAGACTTTA 267  
Db 178 CAGCTGCATAGACTGAGTTCTGGGAAAGAAATGAAGTTATATTTTGTCTCAGACCTTA 237  
Qy 268 CACATAGGAAGTTTACACCTGCTCCGCCCAATCCCGACAAACAGTTCTCTCATCTCCCT 327  
Db 238 CACATAGGAAGTTTACACCTGCTCCGCCCAATCCCGACAAACAGTTCTCTCATCTCCCT 297  
Qy 328 CCGGCTCTCTCCCTCGTGGTGGAAACAAGTAGAAGATGCCACCCCGCTCATAAATTTAC 387  
Db 298 CCGGCTCTCTCCGCCAGTGGGATGGAAACNAAGTGGGAAGATGCCACCCAGTCAATACTAT 357  
Qy 388 GATCTTTTATATGCCATCTCCAAAGCTGGGGCCAGGAGAGAGTATGAAGTGCATGCAGCG 447  
Db 358 GATCTTTTATATGCCATCTCCAAAGCTGGGGCCAGGAGAGTATGAATTCACGACGCG 417  
Qy 448 ACAGACCCCTCTCCAGTGTGGTGTCTCCAGTGTGTGAGAGTGACCAAGAGAAATGAGGAG 507  
Db 418 ACTGACACCACTCCCAAGCTGGTGTCTCATGTATGTGAGAGTGTCAAGAGAAGAGGNA 477  
Qy 508 GAAGAGGAAGAGATGGAGAGATGAAGAGACCCCAAGCCCAAAATCATCCAGACAGGAGA 567  
Db 478 GAAGAGGAA---ATGGAAGAATGAGGAGACCTTAAGTCAAAATTTATCCAGACGAGGAG 534  
Qy 568 CCGGAGTACACACCGATCCACCTTAGCTGA 597  
Db 535 CCGGAGTACACGCGGATCCACCTCAGCTGA 564

RESULT 8  
AA01282  
ID AA01282 standard; cDNA to mRNA; 2174 BP.  
XX  
AC AA01282;  
XX  
DT 09-APR-1999 (first entry)  
XX  
DE Human DSCR1 coding sequence.  
XX  
KW DSCR1; Down's Syndrome critical region 1; human; pathogenic abnormality;  
KW Central Nervous System development; mental retardation; heart defect; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 49..564  
FT FT /\*tag= a  
FT polyA\_signal 1541..1546  
FT FT /\*tag= b  
FT polyA\_signal 2132..2137  
FT FT /\*tag= c  
XX  
PN US5869318-A.  
XX  
XX 09-FEB-1999.  
XX  
PF 07-JUN-1996; 96US-0665040.  
XX  
PR 07-JUN-1995; 95ES-0001140.  
XX  
PA (PALL/) PALLEJA X E.  
XX  
PI Fuentes JJ, Palreja XE, Pritchard M;  
XX  
XX WPI; 1999-152781/13.  
DR



Db 601 TGACACCACTCCCGCGTGGTCCATGATGTGAGAGTGCATCAAGAGAGGAGCA 660  
Qy 510 AGAGGAAGAGATGAGAGAGATGAAGAGACCCAAAGCCCAATCATCCAGACACGGAGACC 569  
Db 661 AGAGGAA--ATGGAAGATGAGGAGACCTAAGCCAAATTTATCCAGACAGGAGGCC 717  
Qy 570 GGAGTACACACCGGATCCACCTTACGTGA 597  
Db 718 GGAGTACACCGCGATCCACCTCAGCTGA 745

RESULT 10  
AAF25338  
ID AAF25338 standard; cDNA; 934 BP.  
AC AAF25338;  
XX 30-APR-2001 (first entry)  
DT Nucleotide sequence of a human detoxification protein.  
DE Human; detoxification protein; DETX; cancer; leukaemia; melanoma;  
XX adenocarcinoma; autoimmune disorder; inflammatory disorder;  
KW rheumatoid arthritis; asthma; atherosclerosis; autoimmune thyroiditis;  
KW psoriasis; ulcerative colitis; infection; cell proliferative disorder;  
KW actinic keratosis; arteriosclerosis; cirrhosis; hepatitis; ss.  
XX Homo sapiens.  
OS  
XX  
PH Key Location/Qualifiers  
FT CDS 20..724  
FT /\*tag= a  
FT /product= "detoxification protein"  
FT sig\_peptide 20..100  
FT /\*tag= b  
FT  
FT  
PN WO200104305-A2.  
XX  
XX 18-JAN-2001.  
XX  
PF 06-JUL-2000; 2000WO-US18509.  
XX  
PR 07-JUL-1999; 98US-0142678.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Tang YT, Yue H;  
XX  
XX WPI; 2001-147193/15.  
DR P-PSDB; AAB31788.  
XX  
XX  
XX New human detoxification protein and polynucleotide, useful for  
PT diagnosis, prevention and treatment of autoimmune/inflammatory  
PT disorders, and cell proliferative disorders including cancer -  
XX  
XX Claim 5; Page 79; 79pp; English.  
XX  
XX The present sequence encodes a human detoxification polypeptide (DETX).  
CC DETX and its (ant)agonists are useful for preventing or treating  
CC disorders associated with decreased or increased expression or activity  
CC of DETX. DETX polypeptides are useful for screening compounds that  
CC specifically binds to DETX and for identifying (ant)agonists.  
CC Diseases prevented, treated and diagnosed include cancers (e.g.  
CC leukaemia, melanoma, adenocarcinoma, cancers of the brain, bone marrow,  
CC breast, kidney, liver, pancreas, prostate and uterus),  
CC autoimmune/inflammatory disorders (e.g. rheumatoid arthritis, asthma,  
CC atherosclerosis, autoimmune thyroiditis, psoriasis and ulcerative  
CC colitis), bacterial, fungal, parasitic infections and cell  
CC proliferative disorders (e.g. actinic keratosis, arteriosclerosis,  
CC cirrhosis and hepatitis). Anti-DETX antibodies may be used as  
CC antagonists, as a targeting or delivery mechanism for bringing  
CC pharmaceutical agents into contact with cells or tissues expressing  
CC DETX and for diagnosis of DETX-related disorders.

XX  
SQ Sequence 934 BP; 247 A; 244 C; 206 G; 237 T; 0 other;  
Query Match 35 38; Score 211; DB 22; Length 934;  
Best Local Similarity 65.28; Pred. No. 3.1e-53;  
Matches 332; Conservative 0; Mismatches 165; Indels 12; Gaps 1;  
Qy 13 GATCTGCAGGACCTGCCGAGGCCACCATCGCTGCCACCTGGAGCCCGCGGTTCGTG 72  
Db 143 GACTTCATGACCTCCCACTCGTTGTTGGTGCAATGTTCCACAGTCTGTTGAA 202  
Qy 73 GACGCCCTGTGCCGGGCCAAATTTGAATCCCTCTTCAGAAACATATGACAGGACACACC 132  
Db 203 GGAGAAAGAGAGCAAGGAAATTTGAGGGACTGTTTCGGACTTATGATGACTGTGTGAGC 262  
Qy 133 TTCCAGTATTTTAAGAGCTTCAACAGTGTCCGGATAAACTTCAGCAACCCCTTATCTGA 192  
Db 263 TTCCAGCTATTTTAAGAGTTCACAGCTGTCCGTATAACTTCAGCAATCTTAATCTGA 322  
Qy 193 GCCGATGCCAGGCTCGGCTGCACAGACCGAGTTCTCTGGGGAAGAAATGAAGTTGAT 252  
Db 323 GCCCGAGCTAGGATAGAGCTTTCATGAACCCCAATTCAGAGGGGAAATAATTAAGCTCTAC 382  
Qy 253 TTTCCTCAGACN-----TTACACATAGGAAGTTACACCTGGCTCCGCCCAAT 300  
Db 383 TTTCACAGGTTTCAGACTCCAGACAGATGGAGACAACTGCACCTTGGCTCCACCCAG 442  
Qy 301 CCGGACAAACAGTTCTCATCTCCCGCTCGGCGCTCTCTCCCGTGGCTGGGAAACAAGTA 360  
Db 443 CCTGCCAAACAGTTTCTCATCTCGCCCGCTTCTCTCCACCTGTTGGCTGGAGGCCATC 502  
Qy 361 GAAGATGCCACCCCGCTCATAAATACGATCTTTTATATGCCATCTCCAAGCTGGGGCA 420  
Db 503 AACGATGCCACGCGCAGTCTCTCAACTATGACCTCTCTATGCTGTGGCCAACTAGSACCA 562  
Qy 421 GGAGAGAAGTATGAACATGCATGCAGCAGACAGACCCCACTCCAGAGTGTGTGTCACGTG 480  
Db 563 GGAGAGAAGTATGAGTCCATGCAGGAGTGTAGTCCACCCCAAGTGTCTGCTGCACGTG 522  
Qy 481 TGTGAGAGTACCAGAGAGATGAGGAGGA 509  
Db 623 TGGACAGTGCATAGAGGAGGAAGAGGA 651

RESULT 11  
ABA91457  
ID ABA91457 standard; cDNA; 3159 BP.  
XX  
XX ABA91457;  
XX  
XX 18-APR-2002 (first entry)  
DT Human Down syndrome critical region 1-like 1 protein cDNA.  
DE Down syndrome critical region 1-like 1; DSCR11L alpha; human;  
XX Down syndrome; Alzheimer's disease; dementia; transgenic;  
KW neuroprotective; nontropic; anticonvulsant; diagnosis;  
KW gene therapy; gene; ss.  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FT CDS 185..952  
FT /\*tag= a  
FT /product= "DSCR11L"  
FT /transl\_except= (pos:215..217, aa:Xaa)  
FT /note= "Xaa = unknown"  
XX  
XX WO200204513-A2.  
XX  
XX 17-JAN-2002.  
XX  
XX 11-JUL-2001; 2001WO-US21982.











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OM nucleic - nucleic search, using sw model

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	597	100.0	597	10	US-09-782-953-2
2	515.8	86.4	597	10	US-09-782-953-5
3	481.8	80.7	2212	10	US-09-782-953-14
4	469	78.6	2358	10	US-09-925-302-347
5	426.2	71.4	599	10	US-09-782-953-1
6	403.8	67.6	2331	10	US-09-782-953-11
7	403.8	67.6	2355	12	US-10-044-090-255
8	399.6	66.9	2173	10	US-09-880-107-3340
9	193	32.3	3184	10	US-09-954-456-497
10	193	32.3	3184	10	US-09-782-953-17
11	186.4	31.2	720	10	US-09-782-953-23
12	186.4	31.2	828	10	US-09-782-953-20
13	183	30.7	594	10	US-09-782-953-8
14	144.6	24.2	412	10	US-09-782-953-10388
15	144.6	24.2	446	10	US-09-864-761-2064
16	123	20.6	486	10	US-09-864-761-809
17	91.8	15.4	111	10	US-09-864-761-27019
18	84.4	14.1	123	10	US-09-864-761-17592
19	81.4	13.6	365	10	US-09-728-445-736

C	20	70.6	11.8	85	10	US-09-864-761-18808	Sequence 18808, A
	21	37.8	6.3	2853	10	US-09-965-631-3	Sequence 3, Appli
	22	37.8	6.3	3446	10	US-09-965-631-7	Sequence 7, Appli
	23	36.2	6.1	5739	10	US-09-960-253-142	Sequence 142, App
	24	36.2	6.1	6417	10	US-09-962-436-288	Sequence 288, App
	25	36	6.0	267	10	US-09-923-876-1137	Sequence 1137, Ap
	26	35.6	6.0	490	10	US-09-880-107-2261	Sequence 2261, Ap
	27	34.4	5.8	257	10	US-09-923-876-1928	Sequence 1928, Ap
	28	34.4	5.8	497	10	US-09-822-263-35	Sequence 35, Appl
	29	34.4	5.8	4363	10	US-09-764-864-241	Sequence 241, App
	30	34	5.7	345	10	US-09-822-263-17	Sequence 17, Appl
	31	34	5.7	387	10	US-09-920-300A-395	Sequence 395, App
	32	34	5.7	387	12	US-10-033-528-395	Sequence 395, App
	33	34	5.7	497	10	US-09-822-263-33	Sequence 33, Appl
	34	34	5.7	1147	10	US-09-880-107-2311	Sequence 2311, Ap
	35	33.8	5.7	156	10	US-09-864-761-20014	Sequence 20014, A
	36	33.8	5.7	415	10	US-09-864-761-3236	Sequence 3236, Ap
C	37	33.6	5.6	1752	9	US-09-887-552A-1	Sequence 1, Appli
C	38	33.4	5.6	575	10	US-09-864-761-8864	Sequence 8864, Ap
	39	33.4	5.6	20247	10	US-09-764-877-2680	Sequence 21553, A
	40	33.2	5.6	299	10	US-09-864-761-21553	Sequence 2442, Ap
C	41	33.2	5.6	470	10	US-09-864-761-2442	Sequence 56, Appl
	42	33.2	5.6	1875	9	US-10-001-835-56	Sequence 56, Appl
C	43	33.2	5.6	2289	10	US-09-850-964-3	Sequence 3, Appli
	44	33	5.5	193	10	US-09-864-761-26305	Sequence 26305, A
	45	33	5.5	466	10	US-09-864-761-5668	Sequence 5668, Ap

## ALIGNMENTS

### RESULT 1

US-09-782-953-2  
; Sequence 2, Application US/09782953  
; Patent No. US20020150953A1  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, R. SANDERS  
; APPLICANT: ROTHERMEL, BEVERLY  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE  
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)  
; FILE REFERENCE: UTSID:674P21  
; CURRENT APPLICATION NUMBER: US/09/782,953  
; CURRENT FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/216,601  
; PRIOR FILING DATE: 2000-07-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 597  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(594)  
US-09-782-953-2

Query Match	100.0%	Score 597;	DB 10;	Length 597;
Best Local Similarity	100.0%	Pred. No. 2.7e-177;		
Matches 597;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGAGGAGGTGGATCTGCAGGACCTGCGAGCGCCACCATCGCTGCGCACCTGGACCG 60		
Db	1	ATGGAGGAGGTGGATCTGCAGGACCTGCGAGCGCCACCATCGCTGCGCACCTGGACCG 60		
QY	61	CCCGTGTTCGTGGAGCGGCTGTGCGGGGCAATTTGAATCTCTTCAGACATATGAC 120		
Db	61	CCCGTGTTCGTGGAGCGGCTGTGCGGGGCAATTTGAATCTCTTCAGACATATGAC 120		
QY	121	AAGGACACACCTCCAGTATTTAAGAGCTTCAACAGTGTCCGGATAAATTCAGCAAC 180		
Db	121	AAGGACACACCTCCAGTATTTAAGAGCTTCAACAGTGTCCGGATAAATTCAGCAAC 180		
QY	181	CCCTTATCTGCAGCGCATGCCAGGCTGCGGCTGCACAAGACCGAGTTCTCTGGGAAGAA 240		

181	Db		CCCTTATCTGCAGCGATGCCAGGCTGGGCTGCACAAGACCAGATTCTCTGGGGAAGCAA	240
241	Qy		ATGAAGTTGTATTTTGGCTCAGACGTTTACACATAGGAAGTTTCACACCTGGCTCGGCCCAAT	300
241	Db		ATGAGTTGTATTTTGGCTCAGACGTTTACACATAGGAAGTTTCACACCTGGCTCGGCCCAAT	300
301	Qy		CCGCAAAACAGTTCCTCATCTCCCTCGGGCCTCTCTCCGTTGGCTGGAACAAGTA	360
301	Db		CCGCAAAACAGTTCCTCATCTCCCTCGGGCCTCTCTCCGTTGGCTGGAACAAGTA	360
361	Qy		GAGATGCCACCCCGCTCATAAATACGATCTTTTATATGCCATCTCCAAGCTGGGGCCA	420
361	Db		GAGATGCCACCCCGCTCATAAATACGATCTTTTATATGCCATCTCCAAGCTGGGGCCA	420
421	Qy		GGAGAGAAGTATGAAGTGCATCGAGCGACAGACCCCACTCCCAAGTGGTGGTCCACGTG	480
421	Db		GGAGAGAAGTATGAAGTGCATCGAGCGACAGACCCCACTCCCAAGTGGTGGTCCACGTG	480
481	Qy		TGTCAGAGTACCAACAGAGATGAGGAGGAAGAGGAGAGATGGAGAGAATCAAGAGACCC	540
481	Db		TGTCAGAGTACCAACAGAGATGAGGAGGAAGAGGAGAGATGGAGAGAATCAAGAGACCC	540
541	Qy		AAGCCCAAAATCATCCAGACACGGAGACCGGAGTACACACCGATCCACTTAGCTGA	597
541	Db		AAGCCCAAAATCATCCAGACACGGAGACCGGAGTACACACCGATCCACTTAGCTGA	597

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RESULT 2
US-09-782-953-5
; Sequence 5, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSID:674P21
; CURRENT APPLICATION NUMBER: US/09782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(594)
; US-09-782-953-5

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	Query Match Best Local Matches	85.4%; Similarity 94.4%; 535; Conservative	Score 515.8; P: 0.74e-132; Mismatches 32;	DB 10; Indels 0; Gaps 0;	Length 597;
Qy	31	AGCGCCACCATCGCCTGCACCTGACCGCGCGTGTCTGTGGAGCGGCCTGTGCGCGGCC	90		
Db	31	AGCTCCCTGATGTCTGTGCGAAACGATGATGCTTTCAGCGAAAGTCAGACCAAGGCC	90		
Qy	91	AAATTTGAAATCGCCTTTCAGAACATATGACAAGGACACCACTTCCAGTATATTTTAAAGAC	150		
Db	91	AAATTTGAAATCGCCTTTCAGAACATATGACAAGGACACCACTTCCAGTATATTTTAAAGAC	150		
Qy	151	TTCAAACGTTCCGGATAAATTTACGAACCCCTTATCTGCAGCCGATGCCAGGTTGCGG	210		
Db	151	TTCAAACGTTCCGGATAAATTTACGAACCCCTTATCTGCAGCCGATGCCAGGTTGCGG	210		
Qy	211	CTGCACAGACCGAGTTCTCTGGGGAAGAAATGAAGTTGTATTTTGTCTCAGACTTTTACAC	270		
Db	211	CTGCACAGACCGAGTTCTCTGGGGAAGAAATGAAGTTGTATTTTGTCTCAGACTTTTACAC	270		

Qy	271	ATAGGAAGTTACACCTGGCTCCGCCCAATCCCGACAACAGATTCCATCATCTCCCTCCG	330
Db	271	ATAGGAAGTTACACCTGGCTCCGCCCAATCCCGACAACAGATTCCATCATCTCCCTCCG	330
Qy	331	GCCTCTCCTCCGTTGGCTGGAAACAAGTAGAAGATGCCACCCCGTCATAAATTAGAT	390
Db	331	GCCTCTCCTCCGTTGGCTGGAAACAAGTAGAAGATGCCACCCCGTCATAAATTAGAT	390
Qy	391	CTTTTATATGCATCTCCAACTGGGCCAGGAGAGAGATGAACCTGCATGCACGCACA	450
Db	391	CTTTTATATGCATCTCCAACTGGGCCAGGAGAGAGATGAACCTGCATGCACGCACA	450
Qy	451	GACCCACTCCCACTGTGGTGGTCCACGTGTGTGAGAGTGCACCAAGAGAAATGAGGAGAA	510
Db	451	GACCCCACTCCCACTGTGGTGGTCCACGTGTGTGAGAGTGCACCAAGAGAAATGAGGAGAA	510
Qy	511	GAGGAAGAGATGGAGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCACACGAGACCG	570
Db	511	GAGGAAGAGATGGAGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCACACGAGACCG	570
Qy	571	GAGTACACACCGATCCACCTTAGCTGA	597
Db	571	GAGTACACACCGATCCACCTTAGCTGA	597

```

RESULT 3
US-09-782-953-14
; Sequence 14, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: US/09782,953
; CURRENT APPLICATION NUMBER: 60/216,601
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(615)
US-09-782-953-14

```

	Query Match	80.7%	Score 481.8;	DB 10;	Length 2212;
	Best Local Similarity 89.1%;	Pred. No. 7.1e-141;			
	Matches 532;	Conservative 0;	Mismatches 62;	Indels 3;	Gaps 1;
Qy	1	ATGCAGGAGGTGGATCTGCAGAGACTGCGCAGCGCCACCATTCGGCTCGCCACTTGCACCGC	60		
Db	25	ATGCAGGAGGTGGACCTGCAGAGACTGCGCCAGCGCCACCATTCGGCTGTGCACCTTGCAGCGC	84		
Qy	61	CGCGTGTCTGTGGAGCGCCTGCGCGGCCAAATTTTGAATCCCTCTTCAGAACATATATGAC	120		
Db	85	CGCGTGTCTGTGGAGCGGCTGTGCGGGCCAAATTTTGATCCCTCTTTAGGACGTATGAC	144		
Qy	121	AAGGACACCACTTCCAGTATTTTAAAGAGCTTCAAACTGTGCCGATAACTTTCAGCAAC	180		
Db	145	AAGGACATCACTTTCAGTATTTTAAAGAGCTTCAACAGAGTCAGAAATAACTTTCAGCAAC	204		
Qy	181	CCCTTATCTGCAGCGGATGCCAGGCTCGGGCTGCACAAGACCGAGTTCCTCGGGGAAGAA	240		
Db	205	CCCTTCTCCGACAGCATGCCAGGCTCCAGCTCGCATTAAGACTGAGTTCTTCTGGGAAAGGAA	264		
Qy	241	ATGAAGTTGTATTTTGTCTAGACTTTTACACATAGGAAGTTACACCTGGCTCCGCCCAAT	300		
Db	265	ATGAAGTTATATTTTGTCTCAGACCTTACACATAGGAAGCTCACACCTTGCTCCGCCAAT	324		





; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3340
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No.. US20020142981A1 U28833
US-09-880-107-3340

Query Match 66.9%; Score 399.6; DB 10; Length 2173;
Best Local Similarity 87.8%; Pred. No. 4e-115;
Matches 448; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 88 GCCAAATTGATCCTCTTCAGACATATGACAGGACACACCTTCCAGTATTATTAAG 147
DB 58 GCCAAATTGATCCTCTTTAGAGCGTATGACAGGACATCACCTTTTCAGTATTATTAAG 117
QY 148 AGCTTCAACAGGTGTCGGGATAACTTCAGCAACCCCTTATCTGCAGCCCATGCCAGGCG 207
DB 118 AGCTTCAACAGGTGTCAGATAAATTCAGCAACCCCTTCTCCGACGACATGCCAGGCTC 177
QY 208 CGGCTGCACAAGACCGAGTCTCTGGGAGGAAATGAAGTTGTATTTTCTCAGACTTTA 267
DB 178 CAGCTGCATAAGACTGAGTTTCTGGGAAAGGAAATGAAGTTATATTTTCTCAGACCTTA 237
QY 268 CACATAGGAAGTTCACACCTGCTCGGCCAATCCGAGCAACAGTTCCTCATCTCCCT 327
DB 238 CACATAGGAAGTTCACACCTGCTCGGCCAATCCAGCAACAGTTCCTCATCTCCCT 297
QY 328 CCGGCTCTCCCTCCGTTGGCTGGAACAAGTAGAAGATGCCACCCCTCATATAATTAC 387
DB 298 CCGGCTCTCCGCTGAGTGGATGGAACAAGTGGAGATGCCACCCATCATATAACTAT 357
QY 388 GATCTTTATATGCCATCTCCAAAGCTGGGGCCAGGAGAGAAGTATGAATGCATGCAGCG 447
DB 358 GATCTTTATATGCCATCTCCAAAGCTGGGGCCAGGAGAGAAGTATGAATGCATGCAGCG 417
QY 448 ACAGACCCCACTCCAGTGTGTGTGCTCCAGTGTGTGAGAGTGACCAAGAGATGAGGAG 507
DB 418 ACTGACACCACTCCAGGCGTGTGTGCTCCAGTGTGTGAGAGTGATCAAGAGAGGAGAA 477
QY 508 GAAGAGGAGAGATGAGAGAAATGAAGAGACCAAGCCCAAAATATCCAGACACGAGGA 567
DB 478 GAAGAGGAA--ATGGAAGATGAGGAGACCTTAAGCCAAAATATATCCAGACGAGGAG 534
QY 568 CCGGAGTACACACCGCATCCACCTTACGCTGA 597
DB 535 CCGGAGTACACCGCATCCACCTCAGCTGA 564

RESULT 9
US-09-954-456-497
; Sequence 497, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-76

; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 3184
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: US-09-954-456-497

Query Match 32.3%; Score 193; DB 10; Length 3184;
Best Local Similarity 67.4%; Pred. No. 2.7e-50;
Matches 293; Conservative 0; Mismatches 130; Indels 12; Gaps 1;

QY 87 GGCACAAATTGAATCCTCTTCAGAACATATGACAGGACACACCTTCCAGTATTATTA 146
DB 276 GGAAATAATTGGGGAGACTGTTTCGGACTTATGATGACTGTGTGACGTTCCAGCTATTATA 335
QY 147 GAGCTTCAACAGTGTCCGGATAAATTCAGCAACCCCTTATCTGCAGCCGATGCCAGGCT 206
DB 336 GAGTTTCAGACAGTGTCCGTATAAATTCAGCAATCCTAAATCTGCAGCCGAGCTAGGAT 395
QY 207 CGGGCTGCACAAGACGAGTTCCTGGGAGGAAATGAAGTTGTATTTTCTCAGACT-- 264
DB 396 AGAGCTTCATGAACCCCAATTCAGAGGGAATAAATAAGCTCTACTTTCACAGGTCA 455
QY 265 -----TTACATAGGAAGTTCAACACTGGGTCCGCCCAATCCCGACAAACAGTT 314
DB 456 GACTCCAGAGACAGATGGAGCAAACTGGCACTTGGCTCCACCCAGCCTGCCAAACAGTT 515
QY 315 CCTCATCTCCCTCCGCGCTCTCTCCGTTGGCTGGAACAAAGTAGAAGATGCCACCC 374
DB 516 TCTCATCTCGCCCGCTTCTCTCCCACTGTAGCTGGCAGCCCATCAACGATGCCAGCC 575
QY 375 CGTCAATAATTACGATCTTTTATATGCCATCTCCAAAGCTGGGCCAGGAGAGATGA 434
DB 576 AGTCCCTCAACTATGACTCTCTCTATGCTGTGGCCAAACTAGGACCAGGAGAGATGA 635
QY 435 ACTGCATGACGACAGACACCCCACTCCCACTGGTGGTCCAGCTGTGTGAGAGTAGCA 494
DB 636 GCTCCATGAGGAGACTGAGTCCACCCCAAGTGTGCTGTCAGCTGTGCGACAGTGACAT 695
QY 495 AGAGAATGAGGAGGA 509
DB 696 AGAGGAAGAAGAGGA 710

RESULT 10
US-09-782-953-17
; Sequence 17, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS

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; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(637)
US-09-782-953-23

Query Match          31.2%; Score 186.4; DB 10; Length 720;
Best Local Similarity 62.6%; Pred. No. 1.3e-48;
Matches 317; Conservative 0; Mismatches 171; Indels 18; Gaps

QY  4  GAGGAGTGGAATGTCAGGACCTGCGGAGCGCCACCATCGCCCTGCCACCTGGAGCCGCGC 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   56  GAGATGATGGAATTAAGTGAATCTGCCATACCTTTTCTTTCAGAGCGTCCATGAAGCA 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  64  GTGTTCTGTGAGCGCCTGTGCCGGGCCAAATTTGAMPCCCTCTTTCAAGACATATGACAAG 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   116  GTGTGTTGAGGCACGAGAGCAGAGGAAGATTTGAAGCACTCTTACCACATCTATGATGAC 175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  124  GACACCACCTTCCAGTATTTTAAGAGCTTCAAAAGCTCTCGGATATAACTTCAGCAACCCC 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   176  CAGGTTACTTTTCAGCTGTTTTAAAAGCTTTAGAAGATCTCAGAATAAAATTTTCAGCAAA 235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  184  TTATCTGAGCGGATGCCAGGCTCGCGCTGCACAAAGACCGAGTTTCCTGGGGAAGGAAATG 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   236  GAAGCGGCAGCAGAGCGCGGAATAGAACTCCACGAACAGACTTCATATGGCAGAGACTA 295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  244  AAGTTGTAATTTTGCTCAGACTTTACATAGAAAGTTTCACACATGGCTGGCTCCGCCCAATCCC 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   296  AAGCTATATTTTGCACAG-----TCCATATCTCTCGCGCCCGCCAGCCT 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  304  GACAAACAGTTCCTCATCTCCCTCCGCGCTCTCCTCCGTTGGCTGGAACAAGTAGAA 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   338  GTCAAGCAGTTCCTCATCTCCCTCCGCGCTCTCCCGAGTGGGTGGAACACAGACGGA 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  364  GATGCCACCCCGTCATATAATATAGATCTTTTATATGCCATCTCCAAGCTGGGGCCAGGA 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   398  GATGCGATGCGCTGTTATATAAATATGATTTACTCTGTGCTGTTCCAAATTTGGGACCAGGA 457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  424  GAGAAGTATGAATGTCATGCAGCGACAGACCCCACTCCCAGTGTGGTGTCCACGTGTGT 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   458  GAGAATAATGAATTCACGCGGGAACAGAGTCGACAGCCAGCGGTGGTTCATGTCTGTCT 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  484  GAGAGTGACCAAGAAATGAGGAGGA 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   518  GAAAGTGAAGTGAAGAGGAAGAGA 543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-09-782-953-20
; Sequence 20, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: US/09/782,953
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)..(745)
US-09-782-953-20

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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10388
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000054.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.62
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.67
; US-09-864-761-10388

Query Match 24.2%; Score 144.6; DB 10; Length 412;
Best Local Similarity 89.1%; Pred. No. 1.2e-35;
Matches 156; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 87 GGCCAAATTTGAATCCCTCTTCAAGACATATGACAAGGACACCCATTCAGTATTTTAA 146
Db 411 GGCCAAATTTGAGTCCCTCTTAGGACGTATGACAAGGACATCACCTTTTCAGTATTTAA 352

QY 147 GAGCTTCAACGGTGTCCGGATAAACTTCAGAACCCCTTATCTGCAGCCATGCCAGGCT 206
Db 351 GAGCTTCAACGGTGTCCGGATAAACTTCAGAACCCCTTCTCCGACGACATGCCAGGCT 292

QY 207 GCGCTGCACAGACCGAGTTCCTGGGGAAGGAATGAAGTTGATTTTCTCAG 261
Db 291 CCAGCTGCATAAGACTGAGTTCTTGGGAAGGAATGAAGTTATATTTTCTCAG 237

RESULT 15
US-09-864-761-2064/c
; Sequence 2064, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359

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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2064
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000122.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; US-09-864-761-2064

Query Match 24.2%; Score 144.6; DB 10; Length 446;
Best Local Similarity 89.1%; Pred. No. 1.2e-35;
Matches 156; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 87 GGCCAAATTTGAATCCCTCTTCAAGACATATGACAAGGACACCCATTCAGTATTTTAA 146
Db 445 GGCCAAATTTGAGTCCCTCTTAGGACGTATGACAAGGACATCACCTTTTCAGTATTTTAA 386

QY 147 GAGCTTCAACGGTGTCCGGATAAACTTCAGAACCCCTTATCTGCAGCCATGCCAGGCT 206
Db 385 GAGCTTCAACGGTGTCCGGATAAACTTCAGAACCCCTTCTCCGACGACATGCCAGGCT 326

QY 207 GCGGCTGCACAGACCGAGTTCCTGGGGAAGGAATGAAGTTGATTTTCTCAG 261
Db 325 CCAGCTGCATAAGACTGAGTTCTTGGGGAAGGAATGAAGTTATATTTTCTCAG 271

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Job time : 57 secs

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 01:34:13 ; Search time 1973 seconds  
(without alignments)  
4900.510 Million cell updates/sec

Title: US-09-575-580B-2  
Perfect score: 597  
Sequence: 1 atggaggagggtgctgca.....cacgatccaccttagctga 597

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba:\*  
2: em\_esthum:\*  
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4: em\_estmu:\*  
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6: em\_estpi:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
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12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518.4	86.8	520	14	B0749142
2	507.8	85.1	1158	14	BQ895506
3	506.2	84.8	1507	11	AK010696
4	495.6	83.0	753	13	B1148584
5	481.8	80.7	890	9	AL538796
6	481.4	80.6	828	9	AL536447

7	476.6	79.8	956	9	AL556803
8	471.4	79.0	937	12	BE795722
9	469.2	78.6	867	14	BQ427531
10	468.6	78.5	923	9	AL551657
11	465.4	78.0	711	13	BG915568
12	463.4	77.6	950	12	BG782633
13	461.4	77.3	980	12	BG296537
14	461.2	77.3	665	13	B1219142
15	453	75.9	710	10	B8617325
16	445	74.5	827	13	B1102432
17	439.2	73.6	727	13	B1327875
18	426.2	71.4	599	9	AA200984
19	409	68.5	570	10	BE287582
20	405.4	67.9	837	9	AU124628
21	403.8	67.6	939	9	AL546617
22	403.8	67.6	1041	13	BM450020
23	402.8	67.5	718	9	AU131040
24	402.2	67.4	931	9	AL543576
25	401.6	67.3	1014	9	AL559594
26	400.6	67.1	946	14	BQ278576
27	400.4	67.1	875	12	BG574693
28	399	66.8	939	9	AL554686
29	393.8	66.0	740	13	B1463566
30	392.8	65.8	885	9	AL544755
31	391	65.5	906	9	AL544313
32	385.2	64.5	769	13	B1767955
33	383.4	64.2	662	13	B1464521
34	378.6	63.4	1078	13	BM541636
35	367	61.5	710	12	BG475986
36	365.8	61.3	811	12	BG570239
37	364.6	61.1	751	9	AL576189
38	360.4	60.4	526	10	AW957479
39	356.8	59.8	627	13	B1859506
40	354.8	59.4	501	12	BF385073
41	354	59.3	600	14	BM743740
42	351	58.8	400	9	AL362314
43	340.6	57.1	437	10	AW291822
44	337.4	56.5	705	9	AL550372
45	336.2	56.3	1047	12	BG287042

## ALIGNMENTS

RESULT 1  
BQ749142  
LOCUS  
DEFINITION  
BQ749142  
IMAGE:5716539 5', mRNA sequence.  
ACCESSION  
BQ749142  
VERSION  
BQ749142.1  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 520)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE  
Unpublished (1999)  
JOURNAL  
Contact: Robert Strausberg, Ph.D.  
COMMENT  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. James Lin, University of Iowa  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
Seq primer: pYX-5.  
Location/Qualifiers  
EST 17-JUL-2002  
linear  
Mus musculus cDNA clone





QY 87 GGCCAAATTTGAATCCCTCTTCAGACATATGACAAAGGACACACCTTCAGTATTTTAA 146  
Db 54 GGCCAAATTTGAATCCCTCTTCAGACATATGACAAAGGACACACCTTCAGTATTTTAA 113  
QY 147 GAGCTTCAACAGGTGCGGATAACTTCAGCAACCCCTTATCTGACGCCGATGCCAGGCT 206  
Db 114 GAGCTTCAACAGGTGCGGATAACTTCAGCAACCCCTTATCTGACGCCGATGCCAGGCT 173  
QY 207 GCGGCTGCACAAGACCGAGTTCCTGGGGAAGAAATGAAGTTGTATTTTCTCAGACTTT 266  
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QY 447 GACAGACCCCACTCCAGTGTGGTCCACGTGTGTGAGAGTGACCAAGAGAAATGAGGA 506  
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QY 507 GGAAGAGGAAGAGATGGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCAGACACGGAG 566  
Db 474 GGAAGAGGAAGAGATGGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCAGACACGGAG 533  
QY 567 ACCGGAGTACACCGATCCACCTTAGCTGA 597  
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DEFINITION 602911995F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5053246 5',  
mRNA sequence.  
ACCESSION B1148584  
VERSION B1148584.1 GI:14608585  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1144 row: m column: 23  
High quality sequence stop: 751.  
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/clone.lib="NCI\_CGAP\_L19"  
/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI;  
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Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
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Query Match 83.0%; Score 495.6; DB 13; Length 753;  
Best Local Similarity 99.0%; Pred. No. 1.4e-121;  
Matches 509; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 84 CCGGGCCAAATTTGAATCCCTCTTCAGACATATGACAAAGGACACACCTTCAGTATTT 143  
Db 171 CCAGGCCAAATTTGAATCCCTCTTCAGACATATGACAAAGGACACACCTTCAGTATTT 230  
QY 144 TAGAGCTTCAACAGTTCGGGATAACTTCAGCAACCCCTTATCTGACGCCGATGCCAG 203  
Db 231 TAAGAGCTTCAACAGTTCGGGATAACTTCAGCAACCCCTTATCTGACGCCGATGCCAG 290  
QY 204 GCTGGGCTGCACAAGACCGAGTTCCTGGGGAAGAAATGAAGTTGTATTTTCTCAGAC 263  
Db 291 GCTGGGCTGCACAAGACCGAGTTCCTGGGGAAGAAATGAAGTTGTATTTTCTCAGAC 349  
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QY 384 TTACGATCTTTTATATGCCAATCTCCAAGCTGGGCCAGGAGAGATGATGAATGCAATG 443  
Db 470 TTACGATCTTTTATATGCCAATCTCCAAGCTGGGCCAGGAGAGATGATGAATGCAATG 529  
QY 444 AGGACAGACCCCACTCCAGTGTGGTGGTCCACGTGTGTGAGAGTGACCAAGAGAAATGA 503  
Db 530 AGGACAGACCCCACTCCAGTGTGGTGGTCCACGTGTGTGAGAGTGACCAAGAGAAATGA 589  
QY 504 GGAGGAAGAGAGAGATGGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCAGACACG 563  
Db 590 GGAGGAAGAGAGAGATGGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCAGACACG 649  
QY 564 GAGACCCGGAGTACACCGATCCACCTTAGCTGA 597  
Db 650 GAGACCCGGAGTACACCGATCCACCTTAGCTGA 683  
RESULT 5  
LOCUS AL538796 890 bp mRNA linear EST 16-FEB-2001  
DEFINITION AL538796 LTI\_FL013\_FBrnl Homo sapiens cDNA clone CS0DF037YL22 5  
prime, mRNA sequence.  
ACCESSION AL538796  
VERSION AL538796.1 GI:12867423  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 890)  
AUTHORS Li, W.H., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).  
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/db\_xref="taxon:9606"  
/clone="CS0DF037YL22"

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REFERENCE
1 (bases 1 to 828)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 131 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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week, 24 week and 46 week))
/lab_host="DH108"
/notes=Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      194 a      235 c      261 g      137 t      1 others
ORIGIN
Query Match      80.6%; Score 481.4; DB 9; Length 828;
Best Local Similarity 88.9%; Pred. No. 9.1e-118;
Matches 531; Conservative 1; Mismatches 62; Indels 3; Gaps 1;

Qy      1  ATGAGAGAGGTGGATCTGCAGGACCTGCGAGGCCACCATCGCCTGCCACCTGGAGCCG 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      216 ATGAGAGAGGTGGACCTGTCAGGACCTGCCAGGCCACCATCGCCTGCCACCTGGAGCCG 275

Qy      61  CGCGTGTTCTGGAGCGCCCTGTGCGGGGCCAAATTTCAATCCCTTCTCAGAACATATGAC 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      276 CGCGTGTTCTGGAGCGCCCTGTGCGGGGCCAAATTTGAGTGCCCTCTTTAGACGTATGAC 335

Qy      121 AAGGACACCACTTCCAGTATTTTAAGAGCTTCAAAAGTGTCCGGATATAAATCTTCAGCAAC 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      336 AAGGACATCACTTTCAGTATTTTAAGAGCTTCAAAAGAGTCAGAAATAAACTTCAGCAAC 395

Qy      181 CCCTTATCTGACCGGATGCCAGGCTGGGCTGCACAAGACCGAGTTCCTGGGGAAGGAA 240
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      396 CCTTCTCCGACGAGATGCCAGGCTCCAGCTGCATGAAGACTGAGTTTCTGGGAAGGAA 455

Qy      241 ATGAAGTGTGTTATTTGCTCAGACTTTACATAGGAAGTTACACACTTCCGCTCCGCCCAAT 300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy      301 CCGGACAAACAGTTCCTCATCTCCCTTCGGGCTCTCCTCCGTTGGCTGGAACAAGTA 360
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      516 CCAGACAAAGCAGTTTCTGATCTCCCTTCGGGCTCTCCGCGAGTGGATGGAACAAGTG 575

Qy      361 GAAGATGCCACCCCGTCATAAATTCAGATCTTTATATGCACTCTCCAAGCTGGGGCCA 420
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DB	576	GAAGATGGACCCCGAGTCATAAACTATGATCTCTTATATGCGCATCTCCAAAGCTGGGGGCCA	635
QY	421	GGAGAGAAGTATGAACTGCAATGACGACAGACACCCCACTCCCACGTGGTGGTCCACGTG	480
DB	636	GGGAAAAGTATGAATTTGCACGACGCACTGACACCACTCCCACCGTGGTGGTCCATGTA	695
QY	481	TGTGAGAGTGCACCAAGAGAATGAGGAGGAAGAGAGATGGAGAAGTCAAGAGACCC	540
DB	696	TGTGAGAGTGATCAAGAGAGGAGGAAGAGAGAA---ATGGAAAGAATCAGGAGACCT	752
QY	541	AAGCCCCAAATCATCCAGACACGGAGCCGGAGTACACCCGATCCACCTTAGCTGA	597

Db	549	GAAGATCGGACCCAGCTCATAAACTATGATCTCTTATATGCCATCTCCAAGCTGGGCSA	708
QY	421	GGAGAGAAGTATGAAGTGCATGAGCAGACAGACCCCACTCCAGTGTGGTGGTCCAGTG	480
Db	709	GGGAAAAGTATGAATTTGCACGACGCACTGACACCACTCCCAAGCTGGTGGTCCATGTA	768
QY	481	TGTCAGAGTCACCAAGAGAATGAGGAGGAAGAGAGATGGAGAGAATGAAGAGACCC	540
Db	769	TGTGAGAGTATGATCAARARARAGGAGAGAGAGAA---ATGGAAGAAGATCAGGAGACCT	825
QY	541	AAGCCCAAAATCATCCAGACAGCAGGACCGGAGTACACACCGATCCACCTTAGCTGA	597
Db	826	AAGCCAAAATTTATCCACACAGGAGCGGAGTACACGCGGATCCACCTCAGCTGA	882
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DEFINITION		mRNA sequence.	
ACCESSION	BE795722		
KEYWORDS	BE795722.1	GI:10216920	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 937)		
COMMENT	NTM-MGC http://mgc.nci.nih.gov/.		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: DCTD/DTP		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov		
	Plate: LLCM802 row: k column: 08		
	High quality sequence stop: 812.		
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	EcoRI; cDNA made by oligo-dT priming. Directionally		
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	adaptor: GGCACGAG(G). Size-selected >500bp for average		
	insert size 1.8kb. Library constructed by Ling Hong in		
	the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using 2AP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	215 a 244 c 286 g 192 t		
ORIGIN			
Query Match	79.0%;	Score 471.4;	DB 12; Length 937;
Best Local Similarity	89.1%;	Pred. No. 4.5e-115;	
Matches	532; Conservative	0; Mismatches	61; Indels 4; Gaps 2
QY	1	ATGAGGAGGTGGATCTCGAGAACCTGCGGACGCCACCACTGCCCTGCCACCTGGACCCG	60
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QY	61	CGCGTGTTCGTGACGGCTGTGCGGGGCAAAATTGAACTCCTCTTCAACAATATGAC	120
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QY 121 AAGGACACACCTTCCAGTATTTTAAAGAGCTTCAAAACGTTCCGGGATAAACTTTCAGCAAC 180
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QY 301 CCGCAACAAGCTTCTCATCTCCCTCCGGGCTCTCTCCGTTGGCTGGGAAACAAGTA 360
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Db 337 CCAGACAAGAGCTTCTGATCTCCCTCCGCTCTCCGCTAGTGGGATGGAAACAAGTG 396
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QY 361 GAAGATGCCACCCCGTCAATAATACGATCTTTATATAGCCATCTCCAAAGCTGGGGCA 420
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Db 397 GAAGATGGACCCCGTCAATAATACGATCTTTATATAGCCATCTCCAAAGCTGGGGCA 456
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QY 421 GGAGAGAAGTATGAAGTGCATGACGAGCAGACCCACTCCAGTGTGGTGTCCACGTTG 480
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QY 481 TGTGAGTGCACCAAGAGAAATGAGGAGGAGGAGAGATGAGAGAGATGAAGAGACCC 540
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QY 541 AAGCCCAAAATATCCAGACACGAGACGGAGTACACACCGATCCACCTTACGTGA 597
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RESULT 9
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DEFINITION
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BO427531
ACCESSION
BO427531.1 GI:21166607
VERSION
EST.
KEYWORDS
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SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL3501 row: n column: 10
High quality sequence stop: 626.
Location/Qualifiers
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Site:2; Salt; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
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BASE COUNT
ORIGIN

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Query Match 78.6%; Score 469.2; DB 14; Length 867;
Best Local Similarity 88.8%; Pred. No. 1.7e-114;
Matches 531; Conservative 0; Mismatches 63; Indels 4; Gaps 2;

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Db 155 ATGGAGGAGGTGACCTGCGGAGGCGCCACCATGCCCTGCCACCTGGAGCCCG 214
QY 61 CCGCTGTTCTGGAGCGGCTGTGCGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 120
Db 215 CCGCTGTTCTGGAGCGGCTGTGCGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 274
QY 121 AAGGACACACCTTCCAGTATTTTAAAGAGCTTCAAAACGTTCCGGGATAAACTTTCAGCAAC 180
Db 275 AAGGACACACCTTCCAGTATTTTAAAGAGCTTCAAAACGTTCCGGGATAAACTTTCAGCAAC 334
QY 181 CCCTTATCTGACAGCGATGCCAGGCTGCGGCTGCACAGACCGAGTTCTCTGGGGAAGAA 240
Db 335 CCCTTCTCCGACAGATGCCAGGCTCCAGCTGCATAGAGACTGAGTTCTGGGGAAGAA 394
QY 241 ATGAAGTTGTATTTTGGCTCAGACTTTACACATAGGAAGTTTCAACCTGCTCCGCCCAAT 300
Db 395 ATGAAGTTGTATTTTGGCTCAGACTTTACACATAGGAAGTTTCAACCTGCTCCGCCCAAT 454
QY 301 CCGCAACAAGCTTCTCATCTCCCTCCGGGCTCTCTCCGTTGGCTGGGAAACAAGTA 360
Db 455 CCGCAACAAGCTTCTCATCTCCCTCCGGGCTCTCTCCGTTGGCTGGGAAACAAGTA 514
QY 361 GAAGTGCACCCCGTCAATAATACGATCTTTATATAGCCATCTCCAAAGCTGGGGCA 420
Db 515 GAAGTGCACCCCGTCAATAATACGATCTTTATATAGCCATCTCCAAAGCTGGGGCA 574
QY 421 GGAGAGAAGTATGAAGTGCATGACGAGCAGACCCACTCCAGTGTGGTGTCCACGTTG 480
Db 575 GGAGAGAAGTATGAAGTGCATGACGAGCAGACCCACTCCAGTGTGGTGTCCACGTTG 634
QY 481 TGTGAGTGCACCAAGAGAAATGAGGAGGAGGAGAGATGAGAGAGATGAAGAGACCC 540
Db 635 TGTGAGTGCATCAAGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 691
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DEFINITION
AL551657 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0DI063VH22 5
prime, mRNA sequence.
ACCESSION
AL551657
VERSION
AL551657.1 GI:12889816
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 923)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="placenta"
FEATURES
source

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/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" 6 others

BASE COUNT	210 a	257 c	295 g	155 t
ORIGIN				
Query Match	78.5%	Score 468.6;	DB 9;	Length 923;
Best Local Similarity	88.4%;	Pred. No. 2.5e-114;		
Matches	528;	Conservative	3;	Mismatches 62; Indels 4; Gaps 2;
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Qy	61	CGCTGTGTCGCGGCGCTGTGCGGCGCAAAATTGAATCCCTCTTTCAGAACATATGAC	120	
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Qy	121	AAGGACACACCTCCAGTATTTAAAGAGCTTCAAGGTGTCGCGATAAACTTCAGCAAC	180	
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Qy	181	CCCTTATCTGACGCGGATGCGGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGG	240	
Db	437	CCCTTCTCGGAGCAGATGCGGAGCTCCAGCTCGATGATGATGATGATGATGATGATG	496	
Qy	241	ATGAAGTTGTATTTGCTCAGACTTTACATAGAGAGTTTACACCTGCGCTCCGCCCAAT	300	
Db	497	ATGAAGTTGTATTTGCTCAGACTTTACATAGAGAGTTTACACCTGCGCTCCGCCCAAT	556	
Qy	301	CCGCAACACAGTCTCTATCTCCCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	360	
Db	557	CAGAGACAGATGCTGATCT	616	
Qy	361	GAAGATGCCACCCCGCTCAATAATTACGATCTTTTATATGCGATCTCAACCTGGGGCA	420	
Db	617	GAAGATGCCACCCCGCTCAATAATTACGATCTTTTATATGCGATCTCAACCTGGGGCA	676	
Qy	421	GGAGAGATGTAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	480	
Db	677	GGGAAAGATGTAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	736	
Qy	481	TGTGAGAGTGACCAAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	540	
Db	737	TGTGAGAGTGATCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	792	
Qy	541	AAGCCCAAAATATCCAGACAGGAGCGGAGTACACACCATCCACTTACCTGCA	597	
Db	793	AAGCCCAAAATATCCAGACAGGAGCGGAGTACACACCATCCACTTACCTGCA	849	
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BG915568	711 bp mRNA linear EST 05-JUN-2001			
LOCUS	602815815F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4945346 5',			
DEFINITION	mRNA sequence.			
ACCESSION	BG915568			
VERSION	BG915568.1 GI:14296044			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 711)			
TITLE	NIH-MGC http://mgi.nci.nih.gov/.			
	National Institutes of Health, Mammalian Gene Collection (MGC)			

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cnapbs-r@mail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10891 row: n column: 03  
High quality sequence stop: 711.  
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BASE COUNT	196 a	184 c	183 g	148 t
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Query Match	78.0%;	Score 465.4;	DB 13;	Length 711;
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Qy	84	CCGGCCAAATTTGAATCCCTCTTCAGACATATGACAGGACACCCCTTCAGTATTTT	143	
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Qy	324	CCCTCCGGCCCTCT-CCTCCGCTGGTGGGAACAGTAGAAGATGCCACCCCGTCAATA	382	
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Qy	383	ATTACGATCTTTTATATGCGCATCTCCAGCTGGGCGGAGAGAGAGTATGAAGTGCATG	442	
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Qy	443	CAGGACAGACCCCACTCCCACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	502	
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RESULT 12
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DEFINITION
602107462F1 NCL_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4236038
5', mRNA sequence.
ACCESSION
BF782633
VERSION
BF782633.1 GI:12087669
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 950)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9843 row: k column: 15
High quality sequence stop: 701.
FEATURES
Location/Qualifiers
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Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCL_CGAP Library. |"
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ORIGIN
source
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Best Local Similarity 96.3%; Pred. No. 6.2e-113;
Matches 517; Conservative 0; Mismatches 16; Indels 4; Gaps 4;
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QY 364 GATGCCACCCCGTCATAAATTACGATCTTTTATATGCCATCTCCAGCTGGGGCCAGGA 423
Db 437 GATGCCACCCCGTCATAAATTACGATCTTTTATATGCCATCTCCAGCTGGGGCCAGGA 496
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BG296537
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mRNA sequence.
ACCESSION
BG296537
VERSION
BG296537.1 GI:13059271
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 980)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/notes="Organ: eye; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 265 a 258 c 269 g 188 t
ORIGIN
source
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Best Local Similarity 96.2%; Pred. No. 2.2e-112;
Matches 505; Conservative 0; Mismatches 16; Indels 4; Gaps 3;
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